

SEQUENCE LISTING

<110> Zyskind, Judith.
Forsyth, R. Allyn

<120> GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
ESCHERICHIA COLI

<130> ELITRA.001C1

<140> Unknown
<141> 2004-02-03

<150> 09/492,709
<151> 2000-01-27

<150> 60/117,405
<151> 1999-01-27

<160> 485

<170> FastSEQ for Windows Version 3.0

<210> 1
<211> 159
<212> DNA
<213> E. Coli

<400> 1

caggtggtat gcaaacccaa aatggagacg ggaagctgaa ccagatagtt actggaggtg 60
atcaccagca gatgaaataa cgataaccag aacaacgcct tatacgcttg agtttgcgag 120
aaaacgttca tattgtacct ttttGattaa ccattgggg 159

<210> 2

<211> 696

<212> DNA

<213> E. Coli

<220>

<221> misc_feature

<222> (1)...(696)

<223> n = A,T,C or G

<400> 2

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aaagagctga cgattcaacc gggatgcagt tccggccagg cgtgtgaaaa cgcgctgcgg 120
gtcacctact caaacgttga accgagcgtt ttcgttcaga ctttctcaccg ccgtaatgg 180
ggggaaagcga ccagcggatt ctttgaagtg ccgaaaaacg aaacccaaaga aaatggatt 240
cgctttccg agcgtaaaga gacactgggt gatgtgacgc accgcattct gacagtgcgg 300
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cgttactggg gcttttgcc ngaagcgaat ctggctggc nggcaacgc tatctggatg 480
aacttcgata accaagaagg cgaatggccg aatggtctgc cctaantcgc attggcgnt 540
ccnttaatan ccacttcctt cnctttgtcc ccttatggca acacttaatt tatntaaan 600
taatcncccgg tggctnacaa atccccgcct ttnttaaaa atttccccna anttaagg 660
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<210> 3
 <211> 681
 <212> DNA
 <213> E. Coli

<220>
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 <222> (1)...(681)
 <223> n = A,T,C or G

<400> 3

ctgcagggtta atgtcgccat taaactggcg cagggagcca aagagttgct ccgcttctac	60
ccagtcggca gcgacaacctt gcgttaaagt cgcaaaaatta tcatctgcac tcactgcgtg	120
acgttaagcgg atggagtggc cggaaacctc atagtgaccg cccaccagg ggcctgcata	180
gctttgttagc gtacgcgcgg cattggcaat aagattcaga tactcagact cttccggggc	240
cttcgcccaggc ataaaaagagg aggatgctcg cgtatgcagc aactgctcca gcgcaaattg	300
cagccgcggc tgagtatcac tgaataaagg atcggtttcg tcaatcaaatt gtggctgagc	360
aaatatttcc tgatagctat cggtatcagg aaccaggta cgcctatgca gtttcgtaat	420
ggtcaaagtt gatgtttttt agtctgttgtt caaagccgcn attataccng taaccggcac	480
tacagcacac gtagaaagca cccgacaata ctcctggcat gggcgtaaaa gctcacagga	540
tggagatctt ttcttcactg gcctaaaaag ctgatattct gtaaagagtt acacngtaac	600
attgagatcg ctatgaaata tcaacaactt ggaaaatctt gnaaagcnng ttggaaaatg	660
gaaagtatct ggttaagaag c	681

<210> 4
 <211> 289
 <212> DNA
 <213> E. Coli

<400> 4

ggcagaattt tacgctgacc aatgacgcga cgacgtggca tggaaataact ccgttggtaa	60
ttcaggattt tccaaaactc tacgagttt gtttgacatt taagttaaaa cgtttggcct	120
tacttaacgg agaaccatta agccttagga cgcttcacgc catacttggc acgagcctgc	180
ttacggcttt taacgcccggc gcagtcaagc gcaccacgta cgggtgtggta acgaacaccc	240
gggaggtctt taacacgacc gtcacggatc aggatcacgg agtgcctt	289

<210> 5
 <211> 815
 <212> DNA
 <213> E. Coli

<220>
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 <223> n = A,T,C or G

<400> 5

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aaatatgaag ggggagagcc cttatagacc aggttagtaca cgtttggta gggggcctgc	120
atatggcccc ctttttcact tttatatctg tgcggttaa tgccgggcag atcacatctc	180
cgaggatttt agaatggctg aaattaccgc atccctggta aaagagctgc gtgagcgtac	240
tggcgccaggc atgatggatt gcaaaaaagc actgactgaa gctaacggcg acatcgagct	300
ggcaatcgaa aacatgcgtc agtccgggtc tattaaagca gcgaaaaaaag caggcaacgt	360
tgcgtctgac ggcgtatca aaacccaaaat cgacggcaac tacggcatca ttctggaaagt	420
taactgccag actgacttcg ttgcaaaaaga cgctggtttc caggcgttcg cagacaaagt	480
tctggacgca gctgttgctg gcaaaaatcac tgacgttcaa gttctgaaag cacagttcga	540
agaagaacgt gttgcgtgg tagcgaaaat tggtaaaaac atcaacattc gcccgttgc	600

tgcgctggaa	ggcgacgttc	tgggttctta	tcagcacgg	gcgcgtatcg	gccgttctgg	660
ttgctgctaa	aagcgctgac	gaagaactgg	ttaaacacat	cgttttgcacc	tttggttgcaaa	720
gccaaggccag	aattcagaga	aactttccgc	ttcaccggag	gtcccaccca	cangganccc	780
cgattnntc	agcatggtgg	tcttcctncg	gagtt			815
<210>	6					
<211>	403					
<212>	DNA					
<213>	E. Coli					
<400>	6					
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cgatagaaaac	aagcattgaa	aggcacagca	gttagtcaaacc	agtgtgaaac	gctactggcg	180
ccttacagcg	caaaaaaggct	ggtgactaaa	aagtccacca	ccatcagcct	gatttctcag	240
gctgcaaccg	gaagggttgg	cttatttaac	ttcaacttca	gcccagctt	tttccagagc	300
tttttctagt	gcttctgcgt	cgtcttgct	cacgccttct	ttcagagcag	ccgggtgcaga	360
ttctaccagg	tcttagctt	cttcagacc	caggccagtt	gcg		403
<210>	7					
<211>	149					
<212>	DNA					
<213>	E. Coli					
<400>	7					
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cagattctac	caggtcttta	gcttcttca	gaccaggcc	agttgcgcca	cgtactgctt	120
tgataacagc	aactttgtta	gcgcacgca				149
<210>	8					
<211>	742					
<212>	DNA					
<213>	E. Coli					
<220>						
<221>	misc_feature					
<222>	(1)...(742)					
<223>	n = A,T,C or G					
<400>	8					
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ggacgtcctg	tcgcgtata	ttaagtcgtc	gatagaaaca	agcattgaaa	ggcacagcag	180
tagtcaaaca	gtgtgaaacg	ctactggcgc	cttacagcgc	aaaaaggctg	gtgactaaaa	240
agtcaccaggc	catcagcctg	atttctcagg	ctgcaaccgg	aagggttggc	ttatTTAact	300
tcaacttcag	cggccagctt	ttccagagct	tttttcagtg	cttctcggtc	gtctttgcctc	360
acgccttctt	tcaagcgcgc	cgggtgcagat	tctaccagggt	ctttagctt	tttcagaccc	420
aggccagttg	cggccacgtac	tgctttgata	acagcaactt	tgttagcgcc	agcagcttcc	480
agaattacgt	cgaattcagt	tnnnncttca	gcagcttcaa	ccggggccagc	agctacagct	540
acagcagcag	caagcggaaa	caccgaattt	ttcttccatt	gcagagatca	gttctacaac	600
cgtccattac	agacatagct	gcaactgctt	caatgatttt	gatcttttagt	ggatagacat	660
ttaaatttgtt	cctgaattat	caagaaataa	gtnttatacg	taagccgaaa	tgcgttaaaa	720
aagataactg	ngattaaagc	ag				742
<210>	9					
<211>	421					
<212>	DNA					

<213> E. Coli

<400> 9

agtagtcaaa cagtgtgaaa cgctactggc gccttacagc gcaaaaaaggc tggtgactaa	60
aaagtccacca gccatcagcc tgatttctca ggctgcaacc ggaagggttg gcttatttaa	120
cttcaacttc agcgccagct tcttccagag ctttttcag tgcttctgcg tcgtcttgc	180
tcacgccttc tttcagagca gccgggtgcag atttaccag gtctttagct tctttcagac	240
ccaggccagt tgccgccccgt actgctttga taacagcaac tttgttagcg ccagcagctt	300
tcagaattac gtcgaattca gttttttctt cagcagcttc aaccggggca gcagctacag	360
ctacagcagc agcagcggaa acaccgaatt tttttccat tgccagagatc agttctacaa	420
c	421

<210> 10

<211> 126

<212> DNA

<213> E. Coli

<400> 10

agagctttt tcagtgcgttc tgcgtcgctt ttgctcacgc cttcttcag agcagccgg	60
gcagattcta ccaggctttt agcttcttc agacccaggc cagttgcgcc acgtactgct	120
ttgata	126

<210> 11

<211> 262

<212> DNA

<213> E. Coli

<220>

<221> misc_feature

<222> (1)...(262)

<223> n = A,T,C or G

<400> 11

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tttttcagtg cttctgcgtc gtctttgctc acgccttctt tcagagcagc cgntgcagat	120
tctaccaggc tttagcttc ttccagaccc aggccagttg cgccacgtac tgctttgata	180
acagcaactt tgtagcgcc agcagcttc agaattacgt cgaattcagt tttttcttca	240
gcagctcaa ccggccagc ag	262

<210> 12

<211> 202

<212> DNA

<213> E. Coli

<220>

<221> misc_feature

<222> (1)...(202)

<223> n = A,T,C or G

<400> 12

gcccataaccc tgcagcatcg gcccgtatggc gatcaggatcg gcagaacgcgt gtaccgctt	60
gttaggttgtt ttaccgggtgn tcaagatccgg gaagatgaac acggtagcgcc gacctgcaac	120
cgagagttc ggcgtttgg atnncgcaac gtcagccatt accgcagcgt cgtactgcag	180
cgaccggcg atcatcaggt ca	202

<210> 13

<211> 261

<212> DNA
 <213> E. Coli

<400> 13
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 ctttgcccg gcatgacgcc gggctttttt tattattccg tgacttcag cgtatgtaa 120
 gcaaacttct cgccatcaaa tagcccctga ctggtagtt tttagcgcccc gatcactggc 180
 agagaaaagaa acgccccatctg aataaacggc tcatacggtta acggaccgca ttcacggcg 240
 gccgcttca aggcgtaat t 261

<210> 14
 <211> 224
 <212> DNA
 <213> E. Coli

<400> 14
 ttctttttt cgtcaacggt gtccagaatc attttattta cctcgccccgtta cttatgctga 60
 tttttattat tatggggaaag gtgttattta tgagttcat ttatgccgtta acgacaatga 120
 actcgggaaat tagtataaagc agcgcgagaa taataatcat tgtgcaaatg ctaatttaat 180
 taataactatt taaatattat tttgagcata tgcacataag gttg 224

<210> 15
 <211> 232
 <212> DNA
 <213> E. Coli

<400> 15
 aattcccttc ttttttgcgt caacgggtgtc cagaatcattt ttatttaccc cgggtactta 60
 tgctgatttt tattattatg gggaaagggtgt tatttatgag tttcattttat gccgttaacga 120
 caatgaactc gggaaatttagt ataaggcagcg cgagaataat aatcattgtg caaatgctaa 180
 ttaatttaat actatttaaa tattattttt agcatatgca cataagggttgg 232

<210> 16
 <211> 212
 <212> DNA
 <213> E. Coli

<400> 16
 aatagcgggat atgcacgcct ttctttttt cgtcaacggt gtccagaatc attttattta 60
 cctcggtac ttatgctgtat ttttattattt atggggaaagg tggttattttat gagtttcat 120
 tatgccgtaa cgacaatgaa ctcggaaattt agtataagca gcgcgagaat aataatcatt 180
 gtgcaaatgc taatttaattt aataactattt aa 212

<210> 17
 <211> 433
 <212> DNA
 <213> E. Coli

<400> 17
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 caggccataa atgccaccag aattatcgctc aaccaaccaa ttgctgaaac gccaaggcagc 120
 agcgccccgg agagctgtttt cagttccggcg ggtaaccctt caatccattt gccggccagtc 180
 cacagcaaca ttagtgcctct gtacaaccctt aacgtgccaa ggggtggcaac aatggcaggg 240
 atcttttagcc acgccccatctg gacaccgttg aaaaatccccg cgagcaaaacc aagcagtaaa 300
 gtcgcgacac aagcaacagg tagtgaatat cctgcgttca gtaacatccc caacagcacc 360
 gcgcacattc cggtaatcga acccactgaa acatcaatat tgcgcgttaag cattaccagc 420
 gtcgcgccccca ttg 433

<210> 18
 <211> 658
 <212> DNA
 <213> E. Coli

<400> 18
 cgtgcgcttc cggttgtggc aaccgcgaa atggcgccgc ggtaagtatg gcggggttat 60
 tcctcccccg ttgaggacac cgggttgcga ggttgcattt acgcttaagt gacaaccccg 120
 ctgcaacgcc ctctgttatac aattttctgg tgacgttgg cggtatcgt tttactccgt 180
 gactgtctg ccgcctttt taaaagtgaat tttgtatgt ggtgaatgcg gctgagcgc 240
 cgccgaacag taaaaccaa aaacagtgtt atgggtggat tctctgtatc cggcgttaat 300
 tggtaactgg ttaacgtcac ctggaggcac caggactgc atcacaaaat tcattgttga 360
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 tgggtgtact atcagaacc cagtatttac tgaagatgcc attaacaaga gaaaacaaga 480
 acgggagcta ttaaataaaa tatgcattgt ttcaatgctg gctcggttac gtctgatgcc 540
 aaaaggatgt gcacaatgaa ttcaatgctt gtcgttgc tgacagttt tcttggcc 600
 ggagagccag ttgatattgc agtcaagtgg tcacaggaca atgcaggagt gtatgact 658

<210> 19
 <211> 588
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(588)
 <223> n = A,T,C or G

<400> 19
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 cacgcggAAC agttaaaacc aaaaacagtgtt atatgggtgg attctctgtatccggcgtta 120
 attgttaact ggttaacgtc acctggaggc accaggcact gcatcacaaa attcattgtt 180
 gaggacgcga taatgaaaac gttattacca aacgttaata cgtctgaagg ttgtttgaa 240
 attgggtgtca ctatcgttac cccagtattt actgaagatg ccattaacaa gagaaaacaa 300
 gaacggggc tattaaataa aatatgcatt gttcaatgc tggctcggtt acgtctgatg 360
 cccaaaggat gtgcacaatg aattcagcat ttgtgttgc tctgacagtt tttcttgc 420
 ccggagagcc agttgatatt gcagtcgtt ttcacaggac aatgcangag tgtatgactg 480
 cagcaaccccg aacagaaaaat tcccggtaac tgttaccgg tcgataaaatg tattcaccag 540
 gataatatcg aaatccggc aggtctttaa aacagttccg taataaat 588

<210> 20
 <211> 101
 <212> DNA
 <213> E. Coli

<400> 20
 gatccagcaa gaagatgcgg ttgtaccgtc atcacgcaga tgcgcaaagc tactcagcaa 60
 ctgaccttcc ttcgcaataa gcacgcccatt agcgtcatag a 101

<210> 21
 <211> 465
 <212> DNA
 <213> E. Coli

<400> 21
 tcgcgtgttt accttcaaca tcggtaactt tctggcggat agttcacgg taagcaacct 60

gcggtttacc tacgttcgct tcaacgttga attcacgctt catacggtca acgatgatgt	120
cgggtgcag ttcccccata cccgcgatga tggctcggtt agattcttcg tcagtcata	180
cacggaaaga cgggtcttct ttagccagac ggcccagagc cagacccatt tttcctggt	240
cagcttttgtt ttccgttca actcgatgg agattaccgg ctcaggaaat tccatacggt	300
ccagaatgtat cgccgcaccc gggcacaca gggtgtcacc agtggttacg tcttcagac	360
cgatagcagc agcgatgtcg cccgcgcgaa ctctttgat ctcttcacgt ttgttagcgt	420
gcatctgaac gatacgaccg aaacgctcac gtgcagctt cacgg	465

<210> 22
 <211> 859
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(859)
 <223> n = A,T,C or G

<400> 22

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gaatacccat gtctactacc gggtagcctg ccagcggacc tgcttcagc tgccctgga	180
tacctttatc aacggccggg atgtattcgc caggattac accacctta atgtcggt	240
tgaactcgta gccttcggg ttgaacccg gctccagcgg gatcatgtcg ataacaacat	300
gaccatactg accacgacca ccagactgtt tcgcgtgtt accttcaaca tcggtaactt	360
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attcacfctt catacggtca acgatgtgt cgagggtcag ttcccccata cccgcgatga	480
tggctcggtt agatttcgtc tcaagtccata cacggaaaga cgggtcttct ttagccagac	540
gggccanagc cagaccatt ttccctggt cagcttggt ttccggtaa ctgcgtatgga	600
gattaccggc tcanggaatt tccataccct ccaggaatga tcggcgcatt ccggtaaac	660
angngntacc aggggggtac ntnttttaa nancattgc cagcancgga nttnnccgn	720
gcnaacttc ttggAACNN ttaccgggtt ggtaaccngc cttttaacn atccaaccga	780
aaaagngtta anngccantt ttccngngt tnanntncgg ntccngaa ntaaccncc	840
cgggttnaac ccngnaaaa	859

<210> 23
 <211> 269
 <212> DNA
 <213> E. Coli

<400> 23

ctttcttaaa gccttcttta aaggcgatacg aagcagccag tttaaacgcc agttcagagg	60
agtcacgtc atggtaagaa cgcgaatgtca gacgaaatacc catgtctact accgggttagc	120
ctgccagcgg acctgccttc agtgcgtccct ggataccctt atcaacggcc gggatgtatt	180
cgccaggat tacaccaccc ttatgtcgat tgcataactc gtagccttc ggggttgaac	240
cgggtccag cgggtacatcg tcgataaca	269

<210> 24
 <211> 330
 <212> DNA
 <213> E. Coli

<400> 24

gttttgggaa gatgttaaggc ctaatctgaa tggctgcatt cttgtttaa ggaaaaacga	60
atgactgatt gcccataacct gattaaacgg gtcataaaaa tcatcattgc tgtttacag	120
ctgatccttc tggtcttata acacaaggaa acgtacttaa ggtgcgtccg gtgaaccagt	180
cggacgcacc ttataataact ataaataagt gtctggcag atactatata aattaactta	240

gtgaatgatt atgctaatgt catcaattaa ataaatataa tggcgtaag gctcccagt	300
aatataatta atactctact tccagagtag	330
<210> 25	
<211> 471	
<212> DNA	
<213> E. Coli	
<220>	
<221> misc_feature	
<222> (1)...(471)	
<223> n = A,T,C or G	
<400> 25	
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atgactgatt gccgataacct gattaaacgg gtcataaaaa tcatacattgc tggtttacag	120
ctgatccttc tggtttata acacaaggaa acgtacttaa ggtgcgtcc ggtgaaccag	180
tccggacgcac cttaataaac tataaataaag tgtctggca gatactatat aaattaactt	240
atgtaatgt tatgctaatt tcataattaa aataaataa atggcgtaa ggcttccag	300
taatataatt aatactctac ttccagaga gaatattaaa ttttatccgc gtggtgcatc	360
agcacaaatt tatcccacaa ctgttcttct gtctcgacat gccccccgat cttnacaaa	420
tantattggg ggatnngcc cnccttttgc ncaggttggg gtcntctnat g	471
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<211> 379	
<212> DNA	
<213> E. Coli	
<220>	
<221> misc_feature	
<222> (1)...(379)	
<223> n = A,T,C or G	
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natctgantg gctgcattcc ttgttaagg aaacccgaat gactgattgc cgataacctga	60
ttaaacgggt catcaaaatc atcattgctg ttttacagct gatccttcgt ttcttataac	120
acaaggaaac gtacttaagg tgcgtccgggt gaaccagtcg gacgcacctt taataactat	180
aaataagtgt ctggcagat actatataaa ttaacttagt gaatgattat gctaattgtca	240
tcaattaaat aaatataatg gctttaaggc ttcccagtaa tataattat actctacttc	300
cagagtagaa tattaaattt tatccgcgtg gtgcattcgc acaaattttt cccacaactg	360
ttcttctgtc tcgacatgc	379
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<211> 799	
<212> DNA	
<213> E. Coli	
<400> 27	
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caaaaaacac taaatcaaaa aataatggca ttagaaaata taatgcgaaa acggagggtga	120
aattagttt tttcaatgc gggaaatctc ccggcgaaaa aaccgggaga tggaaatgtg	180
atgggtatca aataaacaac agaggagaaa tttttaacgc agccattcag gcaaatcggt	240
taatcccatt gcctggcga taagttgcgg cttaacgccg ggaagcgtgt cggccagttt	300
caaaccaata tcacgcagca gtttttcgc cggatggta cggaaaaaca gatcgccgaa	360
tccctgcata ccagccagca tcaacgcgcg actgtgcttgc cggctacgcg catagcgacg	420
cagataatgt tactgcccga tggctggat ccgtcgacat gcagccaagc ttggctttt	480
cagcctgata cagattaaat cagaacgcag aagcgtctg ataaaacaga atttgcttg	540

cggcagtagc	gcgggtgtcc	cacctgaccc	catgccgaac	'tcagaagtga	aacgcccgt	600
gcgccccatg	gtagtgtggg	gtctcccat	gcgagagtag	ggaactgcc	ggcatcaa	660
aaaacgaaag	gctcagtcga	aagactggc	ctttcggtt	atctgggtt	tgtcggtgaa	720
cgctctctga	gtaggacaaa	tccgcccgg	gcggatttt	aacgttgca	aacaaccggc	780
ccggaaagg	gtgggggt					799

<210> 28
<211> 636
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(636)
<223> n = A,T,C or G

<400>	28	agggggttt	ttgtggcaa	tgtgcattt	aagttatcg	ctgcagatag	aggagatatt	60
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gtcactctaa	gaggaggaga	aattaggtt	gtattatacg	tttgtgcgc	catgattggc		180	
gwgcaattt	aacttagtgc	tttacatcgc	tattgtctt	atttcttta	attatttat		240	
aaattaaaaa	aacgactgtt	atgtataagc	aaaggctgaa	cgaaaaat	attccaaata		300	
aatgcttgct	taaatctcta	tatccttccc	cgaaaaatga	cacataaaat	tgagatattc		360	
caaaaaagaga	tactacaaat	aaagatgcct	ttattttatt	atttctaata	aaaatagaag		420	
caataaaaaa	taataacaat	gatataaattc	taatgtttt	aaatatattt	tcttttatgt		480	
tagtaatgt	cgttagtatg	tttgattctc	catatattac	gtgtagttt	ttatatacat		540	
ggaaataatt	ntctttatac	tgagacatca	caccatcatc	aaatgaaat	ttgaagatgg		600	
tgttgggtt	gctaaccat	aaaaagagt	cattcg				636	

<210> 29
<211> 757
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(757)
<223> n = A,T,C or G

<400>	29	cagcggtcgt	attttagca	tggtttttta	ttggcggcta	tgctccccg	ggagcataaa	60
gatggaaaaa	acaacgatta	ttatgtatgg	tgtggcgatt	attgtcgta	tcggcactga		120	
gctggatgg	tggtaacgtc	acctctaaa	aatagcaaaag	gctgcctgt	tgcagcc		180	
gtgcaattt	agcgtaact	ttaatcttc	ctgtagataa	atagcacgac	aatcgacca		240	
ataacggcaa	ccacgaagct	gccaattt	aagccatcga	ctttaccaaa	gccaacacgc		300	
gtgctgatcc	atccgcccac	tacggcaccc	actatcccc	gcaggatagt	cataaagaat		360	
ccacccat	ctttacctgg	catgatccac	ttcgccagaa	tacggcaat	aagccaaaa		420	
ataatccatg	acagaatgcc	cattgtttcc	tcacttatct	gttttgcatt	agcgggttag		480	
tcgctgataa	aaagcatagc	acaacatcgg	gagggcaaga	tttgcacga	gcatcacgg		540	
ggttttttt	gcgatggcgc	agaaattgcg	ccatcaacga	tcagtgataa	ttaccaacca		600	
caaacatcat	gttcgtttc	cgtgtat	gaaccgtacg	ggattcacca	gatctttat		660	
cacttcaagc	cggcacttct	ggcaccagca	aagtcatcgg	cgtctctgt	tcataatcga		720	
ccggaaacgc	cattgctggt	attggtgacn	gtcacgg				757	

<210> 30
<211> 392
<212> DNA

<213> E. Coli

<400> 30

aattacagaa aaaggaggca atatcgggta aaggcattag cccgacgaat acgtcgggct	60
acaatattat ttgtgctgca ggtgttttag cggttggatcc acacatc gacatcgatca tcaaactgaa tagccgcctg ctcgtaaatgt tcctaactgga	120
agaccacatc gacatcgatca tcaaactgaa tagccgcctg ctcgtaaatgt tcctaactgga	180
acaccggcgc ggcatcgct ttcatcatcc gcaccattgg gctgggctga tagttggaaa	240
catggtagcg cacgctatat accggccccca gttaacgatg aaagccgttc gccagttcct	300
gcqccctgatg aatcgcgtta tcaatcgctg cttacgcgc tttgtcttta taggcattcg	360
gctgcgccac gcccagcgac acagaacgaa tt	392

<210> 31

<211> 351

<212> DNA

<213> E. Coli

<400> 31

ctatccttga tgaaaccgcg agcaaagata ggtgattacg tcatggttt acagaaaatt	60
acagaaaaag gaggcaatat cggtaaagg cattagcccg acgaataacgt cgggctacaa	120
atattattgt gctgcagggt ttttagcggg ttgttgatcc acagggttcta actggaagac	180
cacatcgacc tgatcatcaa actgaatagc ggcctgctcg taagtttctt gggcggacac	240
cggcgcggca tcggcttca tcatccgcac cattgggctg ggctgatagt tggaaacatg	300
gtagcgcacg ctatataccg gcccagttt acgatgaaag ccgttcgcca g	351

<210> 32

<211> 762

<212> DNA

<213> E. Coli

<220>

<221> misc_feature

<222> (1)...(762)

<223> n = A,T,C or G

<400> 32

aattatgaaa cactgtctgg aatcgtctga atgacggca catttgcgag cacgcattca	60
gtaataacac aggaaactat ttatctacg cgtagcgat agactgcttgc catggcgaaa	120
ggaggttaagc cgacgatttc agcgggacgc tgaaaacggg aagcccctcc cgaggaagg	180
gccataaaata aggaaagggt catgatgaaat ctactcatca tcgtgggtctt ctttgtcata	240
agcttcccccg cttaactaaga ctaccaggc gggggaaacc ccgctctacc ctcactcctg	300
aaagtatgcc ttacgataa gattgtcaat ccgcaggctt tgtagtctgc gatccgtcca	360
gcaaataattc ttgcgagtc gttacgcaat aatcacagag gaaactattt tattcagcg	420
ttagcgatag actgcattca gggcgaaagg aggttaagccg atgatttcag cgggacgctg	480
aaacgggaaa gcctctcccg gagaagaggg ctttaataa gggaaagggtt atgatgaagc	540
acgtcatcat actgggtata ctcttagtga ttagcttcca ggcttactaa gaacaccagg	600
gggagggggaa aacctttcc taaccctcac ttctgaaatt ggggtctatg acgctggcgt	660
tactgcttan cgctaccagt ttgtctgccc tggcggttgt aacgccagat cggtaccgt	720
ttggatattt taatgaaagc cgacaaatca atcancgtga cg	762

<210> 33

<211> 293

<212> DNA

<213> E. Coli

<400> 33

gcacatttgc gagcacgcat ccagtaataa cacagggaaac tattttatct acgcgttagc	60
gatagactgc ttgcattggcg aaaggaggtt agccgacgtt ttcagcgaaa cgctgaaacg	120

ggaaagcccc tcccaggaa gggccataa ataagaaag ggtcatgatg aagctactca	180
tcatcggt gctcttagtc ataagctcc ccgcctacta agactaccag ggccccggaa	240
accccgctc accctactc ctgaaagtat gcctcacga taagattgtc aat	293
<210> 34	
<211> 633	
<212> DNA	
<213> E. Coli	
<220>	
<221> misc_feature	
<222> (1)...(633)	
<223> n = A,T,C or G	
<400> 34	
atttacactt tttacgaaat catggatca ctaacaaaat atcgcttgatc agttatattg	60
tatggcagga aagatatgcg actgatattt cagatcccc aagtggagag tttatgacca	120
ttaaaaataa gatgttgctg ggtgcgcctt tgctggttac cagtgcgc tggccgcac	180
cagccaccgc gggttcgacc aatacctcg gaatttctaa gtatgaggtt agtagttca	240
ttgctgactt taagcatttc aaaccagggg acaccgtacc agaaaatgtac cgtaccgt	300
agtacaacat taagcagtgg cagttgcgtt acctgcccgc gcctgatgcc gggacgcact	360
ggacctatat gggtggcgcg tacgtgttgc tcagcgacac cgacggtaaa atcattaaag	420
cctacgacgg tgagatttt tatcatcgct aaaaaaagcc ccctcatcat gagggggaaa	480
tgcagacacc ttgttatattt ttattatttgc ccacttgctc gtcttgctt gtatagtc	540
gtatccacg ttgattaatg cnggtggctc cagtgcgc aattaactt gtttggatcg	600
aagacgtagt aactggctgg ttatcgaaat tgg	633
<210> 35	
<211> 569	
<212> DNA	
<213> E. Coli	
<400> 35	
tatggcagga aagatatgcg actgatattt cagatcccc aagtggagag tttatgacca	60
ttaaaaataa gatgttgctg ggtgcgcctt tgctggttac cagtgcgc tggccgcac	120
cagccaccgc gggttcgacc aatacctcg gaatttctaa gtatgaggtt agtagttca	180
ttgctgactt taagcatttc aaaccagggg acaccgtacc agaaaatgtac cgtaccgt	240
agtacaacat taagcagtgg cagttgcgtt acctgcccgc gcctgatgcc gggacgcact	300
ggacctatat gggtggcgcg tacgtgttgc tcagcgacac cgacggtaaa atcattaaag	360
cctacgacgg tgagatttt tatcatcgct aaaaaaagcc ccctcatcat gagggggaaa	420
tgcagacacc ttgttatattt ttattatttgc ccacttgctc gtcttgctt ttatagtc	480
tatttcacgt tgattaatgc ggtgcctcc agtgccacg atttaactt gtttgtatcg	540
tagacgtagt aactggctgg tatcgaaat	569
<210> 36	
<211> 338	
<212> DNA	
<213> E. Coli	
<400> 36	
cgtattcaca tcctttgtt ggtgataac atgcgatcg gtattatattt tccggttgta	60
atcttcattt cagcggtcgt atttttagca tggttttta ttggcggtca tgctgcgg	120
ggagcataaa gatgaaaaaa acaacgatta ttatgatggg tgtggcgatt attgtcgatc	180
tcggcactgc ctggatggt ggtaacgtca cctctaaaaa atagcaaagg ctgcgtgt	240
gcagccttg tgcaattaa gcgttaactt ttaatcttcc tgttagataaa tagcagcaca	300
atcgcaccaa taacggcaac cacgaagctg ccaaattt	338

<210> 37
 <211> 375
 <212> DNA
 <213> E. Coli

<400> 37
 ctgaatattt aaaaaggaaa acgacatgaa accgaagcac agaatcaaca ttctccaatc 60
 ataaaaatatt tccgtggagc attttattat tgaatataga ggttaactc cggtaaaaaaaa 120
 caaagaagca ttgaatgcag qaaaaataa tatgccata aaaaacatcg aaagaaaactc 180
 ttttaattta acatgtaaac gcatggtaa tcctccatatac acgggtggag tgttaagaac 240
 atacataaaat ggagtcatgt tttcccttt ccatttatca agttcctgtt gccgttttag 300
 tccatctcta attgcatatt ttaattttc tgataaaatgg cattgagcat cgatttcatt 360
 taaaacaact gtaca 375

<210> 38
 <211> 446
 <212> DNA
 <213> E. Coli

<400> 38
 ttacgatagc tattagtaaa aatataagag ttagctgtat tgttatgtct gtggcgaat 60
 tgactacctt cgttttttt attaagaatg attttattat cgtaagtaaa attacatgaa 120
 tatttaaaaaa ggaaaacgac atgaaaccga agcacagaat caacattctc caatcataaa 180
 atatttcgt ggagcatttt attattgaat atagaggttt aactccggta aaaaacaaag 240
 aagcattgaa tgcagggaaa aataatatgg ccataaaaaa catcgaaaaga aactctttta 300
 atttaacatg taaacgcattt gttaatcctc atatcacggg tggagtgtt agaacataca 360
 taaatggagt catgtttcc cttttccatt tatcaagttc ctgttgccgt tttagtccat 420
 ctctaattgc atatttaat ttttct 446

<210> 39
 <211> 392
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(392)
 <223> n = A,T,C or G

<400> 39
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 gaaaaacaaa gagataaaatg tctaattcctg atgcaaatcg agccgatttt ttaatcttta 120
 cggacttttta cccgcctggg ttattaattt cactgttnatc cgggcgttcg cccgctttaa 180
 tcacaatagg ctgtgttagcc tgggcctgtt tctcttcac ccgcgcggcaga gcggcagcaa 240
 tcgcattttt atctttggct gcaggttgaa cggctgcgct cttatgtcgt tcaaggcgag 300
 ccgccttttc ggcgcctccaga cggcgtccggc ggcgcctcgaa acgcgcctttg gcttctgcgg 360
 cncgcttttc ttccctgacga atagccgcaa tt 392

<210> 40
 <211> 208
 <212> DNA
 <213> E. Coli

<400> 40
 taataacgct atctgcggat aaagcagaat aggtggtaa ccccagacat aaaccgagga 60
 aaataatgtt attgtatttc ataatctatt gttcccttagc gacagattgc tgtctgtgg 120
 ttcagtaagg taccaggaga aacttcagga agcttgtact cgacaataca gtttgagttt 180

ttatcttgc cccatgaaac ctgtaatt	208
<210> 41	
<211> 342	
<212> DNA	
<213> E. Coli	
<400> 41	
catcctcaat accgttaaat gcaacccgaa cccccgttgt cccttgctg cattcactta	60
acgtaatctg aaaagggacg gctggacttg tgctaccgt cgttggaaat tgctggcac	120
tgttttttttggagatctacg gtaaaattaa gcgaatccga tgagactgtg cagccataat	180
cgaggacgcg cccgctaatt ttaataaacgc tatctgcgga taaagcagaa tagtggtta	240
accccagaca taaaccgagg aaaataatgt tattgttattt cataatctat tgttccttag	300
cgacagatttgcgtg gttcagtaag gtaccaggaa aa	342
<210> 42	
<211> 841	
<212> DNA	
<213> E. Coli	
<220>	
<221> misc_feature	
<222> (1)...(841)	
<223> n = A,T,C or G	
<400> 42	
agatttactg ccaatttccg gcagatcggaa aagggttaaa ccatattgtt ccataagggt	60
acgaatcacg gctataccgc caggcatggc ttgagccatg gcattaaatt ccgc当地attc	120
ggcgctgtat tcttcccacg cggttattttt ggcacacacc agatccagca aggggttntc	180
agatcggttgc acgacgacat gatctaccag ttncagcgcc tgggtgtatt gntcctgtt	240
ctgaataaccc gnnagaaaag gtgccacagc anttagctt tctcctgtt gcaagatgtc	300
tggcaatngc aatcattttt tgcacttant acgatgnaca ncngttaaaga aatcgnattt	360
ttntatgccc tcataactttt acgtatgtt cacttttgc nattcnaaaa aagaccattt	420
gctncaacac gtaaatttta ttgncccnna cattanaac ataaatgntt aaaattttcc	480
ccccncnnan ttttaagnntt ttnanagaat nggaaatttcc ctgcttttta atgnactcan	540
anttttttng naataattcc tntatcnaan ctnnttttcc cccaanagnnc nnccaaattt	600
cggtttntn nttnncnngg ctttttttta cccnanaann tttattcaan nccttttttgc	660
tagnctattt naagnggnt ttnttnattt aactttccnn ttggncaaat tttggcnnat	720
tttatatan aattntctta tntcctaatt tnggnanc cngatgnaan tttatggngg	780
gantcccnnt ccctntttaa tnnatgntct gggntatttt taaancctnn attaannnn	840
c	841
<210> 43	
<211> 215	
<212> DNA	
<213> E. Coli	
<400> 43	
aataactttt cgtaggcag ttttgggtgt gagttgcaag aggggagact actgaataac	60
tcaagtttta taatcgaggg gaaaatgggt atggcgttca tagcaaaacg ccctcaacca	120
taaaggtcga gggcgcttaa gatgttaaaa acccgctatc cgtaaaaaaa caatgttcaa	180
ctaaggtcag tgacattgcg ctaaaaaagc gaatt	215
<210> 44	
<211> 395	
<212> DNA	
<213> E. Coli	

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<220>
<221> misc_feature
<222> (1)...(395)
<223> n = A,T,C or G

<400> 44
gcattattca tgagaaatgt gtatcgaaa tcaactgaaa ttaacgcaac catttggat      60
ttaagggtta attatctgtg tgtgatattt tattgaatgt tttaaatatt gtttttattg      120
gcattgctat aatattgggt atcatttgcg gaatggattc agtcttaatg agtgggttt      180
taagggacag gcatagagta atgatacgtt tgccataacca acatcttac tcattatgtc      240
atgaaatgtt gaccctatgt gtttatgaag gagaggtatt ttcagttgtat ctggatttgt      300
aaattcatat aatgcgcctt tgctcatgaa tggatgccag tatgttagtgg gaaattataa      360
atattgaaat agtccaacta cttcttattt accaa                                395

<210> 45
<211> 883
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(883)
<223> n = A,T,C or G

<400> 45
ataatcaggt aagaaaaagggt ggcggagat taccgtgtgt tgcgatatat ttttagttt      60
cgcgtggcaa tacatcgtg gcaataaaac gacatatacc gaaaaatata cactaagtga      120
atgatatactt ccgatttac ttaatcggtt atggataacg gcaaagggtc tcgtttttc      180
ctataacttac tcagcactca caaataaagg aacgccaatg aaaattatac tctgggctgt      240
attgattatt ttcctgattt ggctactgtt ggtgactggc gtatttaaga tgatatttt      300
aaattaatta atgtcatcgt gtcggaaat aacgagaata tttcagtctc tcattctgtt      360
gcccgtccgt catgtgcatt gcttcataata atcactggcg caaggagcgc cgcaggcna      420
gnntgcncgn cgncccacct nacccatgc cgaacttcgt aantgaaaac ncncntaacnc      480
cgatngtcgg cgggngcctc cccatgcna agtangggaa ntgcccangc ncnnattaaa      540
cgaaaggctn attncaaaga ctgggcctt cnnttatctg atgtttgctg gagaacgctc      600
tcctgagnan gacaaatncc gcccggagcg gatttgaacn ttgcgaagca accgnccna      660
agggngnngt cngacnccc nnctctancn nncngcctc tttgcttna angnccctc      720
ancngatggc cttttngcc ntctaccaaa cnnttggtt aatgcttna aaanccttc      780
cannntncaa tccngtnntn cccatccnnn tnntgaaaagn ntnccnccn tgtncantnt      840
anntnngggg gnngngngcc ggccggcccc cccccccccccc ccc                                883

<210> 46
<211> 1024
<212> DNA
<213> E. Coli

<220>
<221> misc_feature
<222> (1)...(1024)
<223> n = A,T,C or G

<400> 46
gtttatggat aacggcaaag ggcttcgtt tttccataac ttattcagca ctcacaaata      60
aaggaacgccc aatgaaaatt atactctggg ctgttattgtat ttttcctg attgggctac      120
tgggtgtac tggcgtatattt aagatgatatt tttaaaaatta attaatgtca tcaggtccga      180
aaataacgag aatatttcgt tctctcatcc tggcgtccgtc ctgtcatgtc cattgcttca      240

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tataatcact ggcgcaagga ggcgcgagag tnctccnnt nnnnntnntt ntntnnctnn	300
nccttcacna tncnnccncn nantnnatag nnccacnnntn ttntcnlnnn gnccnctcc	360
nnncnnnnnn ncatnnnatc ccactnnntt tnctccannc nnnccnnntn canccnacaa	420
antncnacccn anntnacccn atacnnannc nancnnnnn nnccactctn nctcgnnctc	480
cccnnttcacn ncncannnnn cancnntcnn cttnnnccct nncntaattt ttctnnctan	540
ntcctancen cnacnncc cancnatccn nnatnacant cnattnntn cnntcnctn	600
cnccnnttcc nnctnnncnc tnccncatnc ccnnannan canntncccc ncctncctna	660
ccncncncnc ccnccatccc nnccnnntn ccnnantnga caannnnat cncnnnnncn	720
nnnnnnncnn tnnncncccn gcncnnccnt nccntcacnc tnnncnncta nannnnntac	780
nntnaccnnt cctnnacnc tnccctnnng antccnacna nttnnnnanc nanaacnctn	840
tnnnnccata atcccacacc acnccntnc ancntntnt ncntcntccc ttctatcnc	900
agctnnnnnt nctntnnnc tnccnccnn cnactncnn nnaccncnn cccantcagt	960
ccacncntccn cnncnnntr nnnchancan ctnncacncn chantaacct nntnncacct	1020
tccccc	1024
<210> 47	
<211> 236	
<212> DNA	
<213> E. Coli	
<400> 47	
atatacacta agtgaatgat atcttccgat ttatcttaat cgtttatgga taacggcaaa	60
gggcttcgtt ttttcctata cttattcagc actcacaat aaaggaacgc caatgaaaat	120
tatactctgg gctgtattga ttatttctt gattgggcta ctgggttgta ctggcgtatt	180
taagatgata ttttaaaattt aattaatgtc atcaggtccg aaaataacga gaatat	236
<210> 48	
<211> 418	
<212> DNA	
<213> E. Coli	
<220>	
<221> misc_feature	
<222> (1)...(418)	
<223> n = A,T,C or G	
<400> 48	
cggagattac cgtgtgttgc gatataatttt ttagttcgc gtggcaatac atcagtgca	60
ataaaaacgac atatccagaa aaataatacac taagtgaatg atatcttccg attnatctta	120
ntcgtttatg gataacggca aagggttcg tttttccta tacttattca gcactcacaa	180
ataaaaggaac gccaatgaaa attatactct gggctgtatt gattattttc ctgattgggc	240
tactgggtgt gactggcgta tttaagatga tattttaaaa ttaattaatg tcacatcggc	300
cggaaaataaac gagaatattt cagtctctca tcctgttgcg ctccctgtcat gtgcattgct	360
tcatataatc actggcgcaa ggagcgcgca nggggcggcc aatcgccgccc ggcccttg	418
<210> 49	
<211> 550	
<212> DNA	
<213> E. Coli	
<400> 49	
ctgcttagtta caggaaacac taatgacaga cagctaaaag ccctgtttaa ttacgttatta	60
caaacagggg atgcccagcg ttttcgtgca tttattgggt agatagcgga acgcgcacca	120
caagaaaagg agaaaactgtat gaccattgtt gacagattac gtgaagaagg cgcaatgcag	180
ggccaaacacg aagaagccct gcttattgtt caggagatgc tggatagagg tttagacaga	240
gagtttagtta tgatgggtac ccgactttca ccagacgatc ttatcgccca aagccactaa	300
tcctgttaaca ccgggaggtt actggcgat gtttgcgtt aaccacatca gcgaacgaca	360

tccggccagcg cctcttctaa atcgtaccag cgaaacgcaa aacccgcgttcc ttccagccgt	420
ttaggcagcg cgcgtgtcc acctaatacc agtactgaag attcgcccat taacagtgcga	480
atggcggtcg cggggacgca caaaatggcc gggcgatgca gcgcattgacc gagcgcattgg	540
gcaaattgtt	550
<210> 50	
<211> 99	
<212> DNA	
<213> E. Coli	
<400> 50	
ttggcatctc ggtgtgccg atcttcatga tatccagccc gccggaaact tcttccaaa	60
cgttttgct gttatccatt gagtcacgga actgcccct	99
<210> 51	
<211> 259	
<212> DNA	
<213> E. Coli	
<220>	
<221> misc_feature	
<222> (1)...(259)	
<223> n = A,T,C or G	
<400> 51	
ccgtgccgag atgatccctgt naccatcatc cgttgtgaag tagtgattca cgacttcaag	60
gcgcctttca aaagggtatt ttggctttga catattaggg gctattccat ttcatcgnc	120
aacaaaatgg gtgcagtaca tactcnntgg aaatcaacac aggaggctgg gaatgccgca	180
gaaatataga ttactttctt taatagtgtat ntgttcacg cttttatttt tnaaaanaagt	240
tnggcttact tcccgggnn	259
<210> 52	
<211> 877	
<212> DNA	
<213> E. Coli	
<220>	
<221> misc_feature	
<222> (1)...(877)	
<223> n = A,T,C or G	
<400> 52	
cagcagagcg cggccttctt cgtcagattt cgccagtagtg gtaatggtaa tatccaaacc	60
acgaacgcgg tcgactttat cgtagtcgtat ttctgggaag atgatctgtcacggacacc	120
catgctgttag ttaccacgac cgtcgaaaga cttagcggac aggccacgga agtcacggat	180
acgaggtaca gcaatagtga tcagggcgtc aaagaactcc cacatgcgtt cgccacgcag	240
agttaacttta cagccgatcg gatagccctg acggattttg aagcctgca cagatttgcg	300
tgcttttgtt atcagcgggtt tttgaccggaa gattgctgcc aggtctgtctgcgttgc	360
cagcagtttt ttgtcagcga tcgcttcacc aacacccatg ttcaggggtga tcttctcgac	420
ccgagggact tgcacatgac aattgttagtt aaactcgtc atgagtttt taactacttc	480
gtctttgttag taatcatgca gtttcgcatt cgtactactc catgtcggtt aacgctctcc	540
ttagtaggac aaatccggcc ggagcggatt tgaacgttgc gaagcaacgg cccggagggt	600
ggcggggcagg acgcccccca taaaactgcca ggcataaat taagcagaag gccatcctga	660
cggatggcct ttttgcgtt ctacaaactc ttttgcgtt ttttctaaat cattcaaata	720
tgtatccgtt catcccatcc tatcgatgt aagctgtcaa acatgagaat ttaatcaatc	780
taaagtttta tggngttaaa ctggggctgg cagntncca atggcttaat cagtnaggg	840
ccctatntta acgaactnng ctanttngg tcaatcn	877

<210> 53
 <211> 291
 <212> DNA
 <213> E. Coli

<400> 53
 tgaacacgca agatacggcc agtgcggcca atgttttg tccttaaac ataacagagt 60
 cctttaagga tatagaatag gggtagt acgcagaat atcgattt attattgcta 120
 gtttttagtt ttgctaaaa atattgttag ttttattaaa tgcaaaacta aattattgg 180
 atcatgaatt tggatgtga tgaataaaa atagggggt atagatagac gtcatttca 240
 tagggttata aatgcgacta ccatgaagg tttaattgaa agtattgggt t 291

<210> 54
 <211> 282
 <212> DNA
 <213> E. Coli

<400> 54
 ttattaaatg caaaaactaaa ttattggtat catgaatttg ttgtatgatg aataaaat 60
 aggggggtat agatagacgt catttcata gggttataaa tgcgactacc atgaagttt 120
 taattgaaag tattgggtt ctgataattt gagctgttct attctttta aatatctata 180
 taggtctgtt aatggatttt atttttacaa tttttgtgt ttaggcataat aaaaatcaac 240
 ccgccatatg aacggcggtt taaaatattt acaacttagc aa 282

<210> 55
 <211> 293
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(293)
 <223> n = A,T,C or G

<400> 55
 cggggtccgg cgctcatcaa caatcgaaaa gcagcaaggg gctgaaacgg gaaagcccc 60
 cccgaagaag gggccttgc taaggaaagg gttatgtga agtcgtcat catactgg 120
 gtgtngttac tgttaagttt cccgacttac taacaactca tcagaggggg gagaatcct 180
 cccttaccct tggcccttta ctctaggtt aaaaaacaac agcgtcaata ggcctgccc 240
 gtacgaagcg agatctgtga accgcttcc ggttagcctt ttttacccgt ttg 293

<210> 56
 <211> 300
 <212> DNA
 <213> E. Coli

<400> 56
 tctgcgttcc gctaaaagggt gcaaatgctc aggacgttgc agcgaaaaatgcgttgc 60
 ggggaaggca aaattgcctc tgggaaaggca ttgcgcgggg tccggcgctc atcaacaatc 120
 ggggggcagc aaggggctga aacgggaaag cccctcccgaa agaagggggcc ttgtataagg 180
 aaagggttat gatgaagctc gtcatac tggttgtgtt gttactgtta agttcccgaa 240
 cttactaaca actcatcaga ggggggagaa atcctccctt acccttgcgttcc cttactctaa 300

<210> 57
 <211> 359
 <212> DNA

<213> E. Coli

<400> 57

caacacagga	ggctggaaat	gccgcagaaa	tatagattac	tttctttaat	agtgatttg	60
ttcacgcctt	tatTTTcac	ctggatgata	agagattcac	tgtgtgaatt	gcattttaaa	120
caggagagtt	atgagctggc	ggcgTTTTA	gcctgcaaAT	tgaaAGAGTA	agagtcttcg	180
gcgggaaatt	atTCCTGcct	tacttacggc	gttgcgcatt	ctcattgcac	ccaaatttat	240
tcttcacaaa	aataataata	gattttatta	cgcgatcgat	tatttatttc	ctgaaaacaa	300
ataaaaaaat	ccccGCCaaa	tggcagggt	cttagattct	gtgctttaa	gcagagatt	359

<210> 58

<211> 700

<212> DNA

<213> E. Coli

<220>

<221> misc feature

<222> (1) . . . (700)

<223> n = A, T, C or G

<400> 58

aacacctttt	ctccctgtttt	tcatagaggg	caacccatgt	cctgacacctgg	gttcggggga	60
caccaaaacg	tgccgagatg	atcctgtAAC	catcatcagt	tgtgaagtag	tgattcacga	120
cttcaaggcg	ctttcaaaa	gggtatTTG	gctttgacat	attaggggct	attccatttc	180
atcgTccaac	aaaatgggtg	cagtacatac	tcgttggaa	tcaacacagg	aggctggaa	240
tgccgcagaa	atataGatta	ctttcttaa	tagtatttG	tttcacgctt	ttatTTTCA	300
cctggatgt	aagagattca	ctgtgtGAAT	tgcataTTAA	acaggagagt	tatgagCTGG	360
cggcgTTTT	agcctgcaaa	ttgaaAGGT	aagagtCTTC	ggcggaaat	tattcccGCC	420
ttacttacgg	cgttgtgcAT	tctcatgca	ccccaaATTa	ttcttcacaa	aaataataat	480
agattttatt	acgcgatcga	ttatttattt	cctgaaaaca	aataaaaaaa	tccccGCCaa	540
atggcagggA	tcttagattc	tgtgtttta	agcagagatt	acaggctggT	tacgttacca	600
gctgccgggc	ctttaACGCC	gctttcgtat	gtgaaggaca	ctttctgacc	ttcgtccaga	660
gattgttaacc	atcggtctgg	atagccnaga	aatgtccaaac			700

<210> 59

<211> 631

<212> DNA

<213> E. Coli

<220>

<221> misc feature

<222> (1) . . . (631)

<223> n = A, T, C or

<400> 59

tggtggcatt gggtgctgga gagagaaaaac ccccgacgt tgcaggtatg cacctgacaa 60
caccacgggg gctaattcttg actcttagacc actcaagaat agccgcgaaa cggtgtcatt 120
acaacacagg cggctatatg acgttcgcag agctggcat ggccttctgg catgatttag 180
cggtcccggt cattgctggc attcttgcca gtatgatcgta gaactggctg aacaagcgg 240
agtaaacgtgt catgcgggcg tcaggctgcc gtaatggcaa ttgcgcggccg gaccaggccg 300
caggggggaa actctgcggc cttttcgtt cttactgcgg gtaaggcacc caagtcgcgc 360
cgttcaggcg aacgtacggt ttatccgtt attgaataac tactgcattt gagttctcg 420
agaccgggtgc tgtttgcggc aacccactgg ttagttttt ccagtcaaca ttgtcttcgg 480
tgaaaatctt gccatcgaga acgcgaacca ccagatcgga gatagccagg aagctgctcg 540
gttgttcgtat gacaatcggt gccccctgtat gcggtgcctt catgccgaag aatttcaccc 600
caacggggac gtcngtataa gaccgggcta q 631

<210> 60
 <211> 648
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(648)
 <223> n = A,T,C or G

<400> 60

ggctcaggcn	tgctgattgt	tttttgtc	aatgccng	tattagcgtc	gttgctgtcg	60
atggagagaa	tcataaacgt	ggtgaatgt	gattgttagc	aaggaaaact	gtcaaaaatc	120
ttcaaaaaat	ttgagggata	aggccggaat	ggctccggcc	agagggaagt	taaccgcgaa	180
gctgttgc	cttgagggtc	gttttaacca	gacgccaggc	gctccatacg	ccaaaaccgc	240
gtctggccca	goggaccagc	atattaggat	ggcgaatcgt	ccagatcgcc	atcacgctac	300
tgccaaccag	cggccaggag	cgcagacta	gcagcatatt	ccancgacga	tcgtaagcgc	360
ctgttgtctc	cagccattca	cgacgactgg	cggaagggnnc	cgcgnctgac	caacttgnct	420
tttagnctga	tncanatttan	attnataaaac	gcagnanncn	ggtntgatta	atcntattn	480
gctctngtct	ggtagttagc	nncggnnngt	ctcnntntna	ccnnttcnn	tttannttac	540
natnngtaan	ttatntttnt	nngtctnnt	tntanttng	tactntaagt	ntatncgnnn	600
atnnntnnnan	nnncagnnc	ntnttttta	aatnntttnt	nanncnnc		648

<210> 61
 <211> 737
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(737)
 <223> n = A,T,C or G

<400> 61

tgctaataatc	tttctcatttgc	agatgaaaat	taaggtaagc	gaggaaacac	accacaccat	60
aaacggaggc	aaataatgct	gggtaatatg	aatgttttta	tggccgtact	gggaataatt	120
ttatttctg	gttttctggc	cgcgtatttc	agccacaat	gggatgacta	atgaacggag	180
ataatccctc	acctaaccgg	ccccttgtta	cagttgtta	caaggggcct	gattttatg	240
acggcgaaaa	aaaaccgcca	gtaaaaccggc	ggtgaatgct	tgcatggata	gatttgtt	300
ttgctttac	gctaacaggc	attttcctgc	actgataacg	aatcgttgc	acagtagcat	360
cagtttctc	aatgaatgtt	aaacggagct	taaactcggt	taatcacatt	ttgttcgtca	420
ataaacatgc	agcgatttct	tccggtttgc	ttaccctcat	acattgccc	gtccgctt	480
ccaatgacca	catccagagg	ctttcagga	aatgcgcgac	tcacac	tgcgttgc	540
atgttgat	gcccttcaga	atgtgtgat	gcatggtat	cgactaactg	gcaaattctg	600
acacctgcac	gacatgttc	ttcatcatta	gcccgttga	caataatgtat	aaattcttgc	660
cccccgtagc	gataaaaccgt	ttcgtatna	cgcgtccaac	tggtntaagt	aaagttgc	720
gggtgccgt	atcttac					737

<210> 62
 <211> 648
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(648)
 <223> n = A,T,C or G

<400> 62	
tgctttgaa tatgtgctcg caatctttag aagggaaatgg cgaccacgaa agaaaaggca	60
aaaaccgata atctgaaaga acccaagtat ttcatgtataa gcattgaatg ccgaccagta	120
aactcttcg gattcaccca gaaagtgaan ccaaaatgtat aatcgatatac ataagtctt	180
cgagtggctc gttagaaaaa agtttcaaca atggagtaaa tacatccaa atatcaataa	240
ctctcaactg taaggggatt gaaatggtaa ccccagctct tcgcttgagg ggtatagccg	300
agaccaccga agccccggag gtggtaaat aaaaccggc acaacacgaa agggcgcatt	360
tccgatatacc ataaaagaag tcgggtctt gtctggtaaa attaaatgg tgggaagtgc	420
gcctccgggt tgtaaataacc gactttgctg ggttagcct ggcggcatca agtttttc	480
tggaaagtgc ctgatgtccg cccttttaa agggatttt ggtgatgccg gtgaatgccg	540
cttaacccccc cgtggccca gttaaaagtc atgtaagnnc ctaatngtt tgggtggga	600
aaagccnact gnnaatttgt tacctggtt gcaagtanc cttggagg	648
<210> 63	
<211> 237	
<212> DNA	
<213> E. Coli	
<220>	
<221> misc_feature	
<222> (1)...(237)	
<223> n = A,T,C or G	
<400> 63	
gggttttant tacaagagat tcatctttgt nttaaancnn gataagtaat tacgcataaa	60
acaacaatga ttataatagc aaaaataat attatcatct ttgatagatt acttgagata	120
gcacatct tgtaaagcct ttatcgaaaa ttatgctct ggattaatat aatcactaca	180
tctatctgag caatctgtt ttgatggaca tgtcaaccca tggcattta cagccaa	237
<210> 64	
<211> 427	
<212> DNA	
<213> E. Coli	
<400> 64	
gataatttgc gtttgcgtc agaaaattga cgttacccat aacaaatgaa aggccaggt	60
aatcatgccca ttatgcattt tgctatcg tgtaatctt tggttgcctc tgatgatccg	120
cttcaaaatg aacggcttca tcgctctcg cctcggtcg cttgctgtg gattaatgca	180
aggaatgccg ctggataaaat ttatggctc catcaaagcc ggtgtcgccg ggacgctcg	240
tagccttgcc ctgatcatgg gtttggcg aatgctggc aaaatgctgg cagactgcgg	300
tggcgacaa cgtatcgcca ccacgctgat tgccaaatgg gttaaaaaac acatccagtg	360
ggcgggtggta ctgaccgggtt ttaccgttgg ttttgcctg ttctatgaag tggccttgc	420
gctgatg	427
<210> 65	
<211> 261	
<212> DNA	
<213> E. Coli	
<220>	
<221> misc_feature	
<222> (1)...(261)	
<223> n = A,T,C or G	
<400> 65	
caaagaacct tcaacatgaa aaatatccat ttgtttgcaa aaaaagatata ttaggaagga	60

aattaatgca attatcgaaa attcaaaaa tatccaaaaa tngtatactt tattccagaa	120
gagttcaata taatgttgt cttcaattt tcttacttca gggtaatata gattgctcat	180
tacattgtga gcttcatctt tatttaattt tctgttgact ccagctctcc gtgataacgg	240
ttttataatt agatgcttat c	261
<210> 66	
<211> 98	
<212> DNA	
<213> E. Coli	
<400> 66	
agatgattgc cgggacttg ttagcggcac gcaggcggcg gctcgacccc ttaccctgct	60
ctttacgtac ttctgcgttg atagtaaaca tttcttgc	98
<210> 67	
<211> 260	
<212> DNA	
<213> E. Coli	
<400> 67	
aagcgcgaac gaagtgcgt tgctgcagct tcgggttgc cgggtgacgc tgtacgtcct	60
gagctttaac tttgatttct ttaccgtcaa caacgatggt cagaacttcg ctgtagaatt	120
cagctttagc ttgcgttgc atgactttgt cgtgatccag ctcgatagcc agccgcgtt	180
cttgcacc gtagatgatt gccggact tggtagcggc acgcaggcgg cggctcgcac	240
ccttaccctg ctcttacgt	260
<210> 68	
<211> 95	
<212> DNA	
<213> E. Coli	
<400> 68	
aaaaacggcg taaagaaaagg ttgcaaacat gttaataaaa actcaaattt atcccacgta	60
tatattacgc cgcaaaatcc ttacaataaa caggg	95
<210> 69	
<211> 174	
<212> DNA	
<213> E. Coli	
<400> 69	
ttaattatta aaatagtgtt acgcgattat gtggatatgg gggtaaacat taaataaacc	60
agcggggagg ggaggtaaag tgaaaaataaaa aaaagcggat aatcttaata agcaggccgg	120
acagcatcgc catccggcac tgatacggg tttatttcag ctcatcaacc atcg	174
<210> 70	
<211> 138	
<212> DNA	
<213> E. Coli	
<400> 70	
agtctgtaaa aacgtcaaaa agagtgttt atcaacagaa gaatggaggt ctgacagata	60
gtagtaatgc aaaaaaatgg agacttaagt tgaatgaacg ggagtaaagc gaaaagacta	120
tagagtgaag gagaaatt	138
<210> 71	
<211> 191	

<212> DNA
 <213> E. Coli

<400> 71
 tttgttggct taatattcta ttgttatctt tatttataga tgtttatatt gcatgagggtg 60
 gttttggag agaagaatga ggaagatgcg tcgagccaca gaaacgttag ctttacatat 120
 acggagggtg atgtgaattt aatttacaat agaaataatt tacatatcaa acagtttagat 180
 gcttttgtc g 191

<210> 72
 <211> 244
 <212> DNA
 <213> E. Coli

<400> 72
 ggccatttat acagggaaaag cctatgtcag aacgtaaaaa ctcaaatca cgccgttaatt 60
 atctcgtaa atgttcctgc ccaaactgca cccaaagagtc agaacacagt ttttcaagag 120
 tacaaaaagg tgccctttg atctgccctc attgcaacaa agtattccag acaaatctta 180
 aagctgttagc ctgatttgatt ttatttagtaa caagtatttt ttatattta ataatatatt 240
 taaa 244

<210> 73
 <211> 327
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(327)
 <223> n = A,T,C or G

<400> 73
 aaattttcag gtaccttgc accatacttt ttttctgag cattaatgat attttgagct 60
 tcttgaggat cttaactcc ccacatttgg tggaaagtat tcataattaaa aggaaggntg 120
 aataatttgn cttaataat cgccagtgg aatttagtaa aacgattaaa ttctactaaa 180
 tnattaaccg naaaaaaatt cccatatata ttatcattt gtatgaaaaa tatgtgcacc 240
 atatttatga atntggatac cctnacagtc ctctgtgtac gcatttccac cgatatgatt 300
 tctttctna atcactaaaa cttttt 327

<210> 74
 <211> 150
 <212> DNA
 <213> E. Coli

<400> 74
 gcagtgtatcg aagcgatgac gaagtgtatg gaaaaatcag aaaaactcag caaatcctga 60
 tgactttcgc cggacgtcag gccgccactt cggtgcgggt acgtccggct ttcttgctt 120
 tgtaaagcgc caaatctgcc gatttcaacc 150

<210> 75
 <211> 330
 <212> DNA
 <213> E. Coli

<400> 75
 gaaagtatct tcgttattga catcaactgga aaatataact tgctttcat tattaaactc 60
 gaagcgcgtc ccgtatctgg acaaacattt atcgagctt ccaaattcct gaagagggtt 120

aactacagat aacatttgcg cgtccttgc agtaatgccc gtcaaatcct tgacgggcat	180
tattttagatt aaatttaccag tatttcttcg gagtgaagaa tattaccagg tatatttaac	240
acccacgttc gcggaccagt ctgtatctac gtcaccacca ccgaggtagt tagcatcggt	300
ataggcgctg aagtttttgg tgaagctaaa	330
<210> 76	
<211> 194	
<212> DNA	
<213> E. Coli	
<400> 76	
tgtttttttc cagcaacgga gcaaaagggtt tgcccttg cagctcaggg ttaaccactt	60
taactacgtg gcgcacgaccc ggagatgtcg gtttacattt aacaactgcc attgtattac	120
tccctcgact tactcagcgc cgccaacgaa gtccagattc tggccttct tcagggtgac	180
gtaagctttt ttcc	194
<210> 77	
<211> 188	
<212> DNA	
<213> E. Coli	
<400> 77	
tcccttaac taccagggtg ttaacgactt cgacttcgac ttcaaacagt ttctgcacag	60
cagctttgat ttctgccttg gtcgcgtctt tagcaacttt gagtactatg gtgttggatt	120
tttccatcgc agtagacgct tttcagaaa cgtgcggc acgcagcacc ttcagcagac	180
gttcttca	188
<210> 78	
<211> 173	
<212> DNA	
<213> E. Coli	
<400> 78	
acaaaggcga acaaaggcctg tgaagccccga aggctccaca gacagtgcata cttgaaggcc	60
ttactgtttc ttcttaggag cgagcaccat gatcatctgg cggccttcga tcttgggtgg	120
gaaggattcg accactgcca gttcttgcaa atcgctttc acgcgattaa gca	173
<210> 79	
<211> 272	
<212> DNA	
<213> E. Coli	
<220>	
<221> misc_feature	
<222> (1)...(272)	
<223> n = A,T,C or G	
<400> 79	
tggagaaaaac ggggtgattga taaagcaatc atcggttctag gggcgtaat tgcgtgcgt	60
gaactgatcc cgctttctgc ttcaagcttc tgaactggat acggaaacgt aatnagggt	120
aaagaagaca ctactcttag ccctttaaca tttaacgcattgtcacgaac tcttctgccg	180
ccgttgggtg aatggcgacg ggtattggtc gaaatcttt ttgggtggcc ccatctttaa	240
cggccaccctg caacatttcg tc	272
<210> 80	
<211> 259	
<212> DNA	

<213> E. Coli

<400> 80

cgcaggcagc tcatggtaaa caggatgaga gaaacccaga gacaggtaa tcacattgcc	60
ttaaccgct gcacgtaac ctacaccaac cagctgcagc ttcttagtga agcctcggt	120
aacaccgata accattgagt tcagcaggc acgcgcggta ccagctgtg cccaacgcgtc	180
tgcgtAACCA tcacgcggac cgaaggtagt ggtattatct gcatgtttaa cttcaacagc	240
atcggtgaga gtacgagtc	259

<210> 81

<211> 73

<212> DNA

<213> E. Coli

<400> 81

caggTCggaa cttacccgac aaggaatttc gctaccttag gaccgttata gttacggccg	60
ccgtttacccg ggg	73

<210> 82

<211> 666

<212> DNA

<213> E. Coli

<400> 82

atgaacgttt tctcgaaac tcaacgctat aaggcgttgt tctggttatc gttatttcat	60
ctgctggta tcaccccgta taactatctg gttcagcttc ccgtctccat tttgggttcc	120
cataccacct ggggcgcgtt tagcttccg tttatTTTC ttgctaccga cctgaccgtg	180
cgtatTTTG ggcgcaccgtt ggcccgcacgc attatctcg cgtaatgtat ccctgcgtta	240
ttaatctcct acgtcatctc gtcgttattc tatatgggtt cctggcaggg attcggcga	300
ctcgccccact tcaacctgtt tgcgtcccgat atcgcaccgc ccagtttcat ggcctacgcg	360
ctggggcaaa tcctcgacgt gcacgtttt aaccgcctgc gtcagagtcg ccgcgtgtgg	420
ctggcaccga cagcgtccac actgttcggt aacgtcagcg acacgctggc ctttttcttc	480
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gtcgattact gttcaaagt gttaatcagt atcgtttct tcctgccaat gtatggcgt	600
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<210> 83

<211> 612

<212> DNA

<213> E. Coli

<400> 83

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<210> 84

<211> 975

<212> DNA

<213> E. Coli

<400> 84

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<210> 85

<211> 1761

<212> DNA

<213> E. Coli

<400> 85

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1761

<210> 86
<211> 1185
<212> DNA
<213> E. Coli

<400> 86

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<210> 87
<211> 2115
<212> DNA
<213> E. Coli

<400> 87

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<210> 88

<211> 540

<212> DNA

<213> E. Coli

<400> 88

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<211> 1549

<212> DNA

<213> E. Coli

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<211> 1767

<212> DNA

<213> E. Coli

<400> 94

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<211> 1227

<212> DNA

<213> E. Coli

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<211> 900

<212> DNA

<213> E. Coli

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<211> 1029
<212> DNA
<213> E. Coli

<400> 100

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<212> DNA
<213> E. Coli

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<212> DNA
<213> E. C.

<400> 102

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<210> 103
<211> 876
<212> DNA
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<400> 103

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caggctatcg	atcaggcgc	ttctgggtgt	gatatggggc	gtaatattt	ccagtcgtac	780
catccgggtgg	cgtatgatgaa	agccgtacag	gcccgtgttc	accataacga	aacggctgat	840
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<210> 104

<211> 291

<212> DNA

<213> E. Coli

<400> 104

atgcacgtca	cactgggtga	aattaacgtt	catgaagaca	aggttgcga	gtttatcgaa	60
gttttcgc	agaaccacct	gggctctgt	caggaagaag	gcaatttgc	cttcgatgtc	120
ttacaggacc	cggaaagtgaa	ttcgcgc	tatatctacg	aagcctataa	agatgaagac	180
gcagtggcg	tccataaaac	cacgc	tacaaaac	gtgtcg	actggaaatct	240
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<210> 105

<211> 1152

<212> DNA

<213> E. Coli

<400> 105

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gcggtaaata	ccgatgcaca	agcgctcg	aaaacagcg	ttggacagac	gattcaa	180
ggtagcggt	tcaccaaagg	actggcg	ggcgcta	cagaagttg	ccgcaatgc	240
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gctcgccgt	tgggttgtt	taccgtaca	gtgcagcac	cagtcgtcg	tgaagtgg	360
aaagatttgg	gtatcctgac	cgttgctgtc	gtcacta	cttcaactt	tgaaggca	420
aagcgatgg	cattcgccg	gcaggggatc	actgaactgt	ccaagcatgt	ggactctct	480
atcaatatcc	cgaacgacaa	actgctgaaa	gttctggcc	gcccgtatctc	cctgcgtgg	540
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cctgaaatca	ctctgggtac	caataa	gttcagc	cagt	gatgg	1020
cagcatggga	tggctccg	gaccc	caggag	cagaag	ccgg	1080
aatgcgcgc	aaactgcgaa	agagccg	gat	tatctgg	ata	1140
caagctgatt	aa					1152

<210> 106
 <211> 3048
 <212> DNA
 <213> E. Coli

<400> 106

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aatgtaaat	gtcagcagg	tgaaacgg	ggtatccaa	tccactgggg	ctttaggg	2940
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caaacgc	aatataa	aggcgt	gttcttag	aacatcg	gaga	3048

<210> 107
 <211> 885
 <212> DNA
 <213> E. Coli

<400> 107

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tctcaggtgc	gtgattacaa	agcagaagtc	gcaaaactta	tcgacgttcc	cacctgtatc	120
ggctgtaaag	cctgtcaggt	ggcgtttcg	gagtggaaacg	acatccgtga	tgaagtgggg	180
cactgcgtcg	gggtttacga	taaccccccc	gatctgagcg	ccaagtccgt	gacgggtatg	240
cgccttagcg	aaaccgaaca	gaacggcaag	ctggagtgcc	tgatccgtaa	agacggctgt	300
atgcactgtg	aagatcccgg	ctgcctgaag	gcgtgcccgt	ctgctgggtc	aatcatttcag	360
tacgctaacg	ggattgtcga	tttccagtcg	gaaaactgca	tcggctgtgg	ttactgcatt	420
gccgggtgtc	cgttaataat	tccgcgcctc	aacaaagagg	ataaccgggt	atataaatgc	480
acgctctgcg	tcgatcgcgt	cagcgtcggc	caggaaccgg	cttgtgtgaa	aacctgtccg	540
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gttacgcacg	ttatgtacgt	gctgcacac	gccgatcagc	cgagactgt	tcacggctcg	720
ccgaaagatc	cgaagatcga	caccccggt	agcctgtgga	aaggcgctt	gaaaccgctg	780
gcagcggctg	gctttattgc	cactttgcc	gggttgattt	tccactacat	cggatttggc	840
ccgaataagg	aagtggacga	tgacgaggag	gatcatcatg	agtaa		885

<210> 108

<211> 654

<212> DNA

<213> E. Coli

<400> 108

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gtgggtgattt	gcttcttcct	ggggcgctg	tccgggattt	cgtttttctt	cccgacgctg	120
caatggctga	cgaaacaccc	cggtacgccc	catatggac	gcattttgca	cccggttctc	180
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cagtacttcc	cgatgcaggt	tgttcgctac	agcctgtga	tccacgcggc	tgccgggtatc	480
atccgtatcc	acgccatcct	gatccatatg	tatatggcat	tttgggtgaa	aggatcgatt	540
aaaggatga	tcgaaggggaa	ggtaagtctgt	cgctggcga	agaaacacca	tccgcgtgg	600
tatcgtgaaa	tcgagaaggc	agaagcgaaa	aaagagatg	aagaaggat	ataaa	654

<210> 109

<211> 261

<212> DNA

<213> E. Coli

<400> 109

atggcggtgt	taatcactaa	aaaatgcac	aattgtgata	tgtgtgaacc	cgaatgcgg	60
aatgaggcga	tttcaatggg	agatcatatc	tacgagatta	acagcgataa	gtgtaccgaa	120
tgcgttagggc	actacgagac	accaacctgc	cagaagggt	gcccgttcc	caataactatt	180
gtgaaagatc	cggcgcatgt	cgagacagaa	gaacagttgt	gggataaatt	tgtgtatg	240
caccacgcgg	ataaaattta	a				261

<210> 110

<211> 1203

<212> DNA

<213> E. Coli

<400> 110

atgcaaagtgttgc	cattgttggc	ggcgcatgg	tggggctggc	ggttgcctgt	60
ggcttacagg	ggagccgctt	acgcgttgc	gtactggagc	agcgcgtaca	120
gccccgaatg	caccaccaca	actgcgcgtt	tcggctatca	atgccgcag	180
ctcacccgtc	ttggcgtctg	gcaggacatt	ctctctcgta	gggccagctg	240
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cgtcaggggaa	aagacatcg	cgactacatt	tatctgcgtc	gctatgagcg	1020
cacagtgcgg	cgttgcgtct	ggctggatgc	caggattcc	gcgatctgtt	1080
aatccggcga	aaaaactgct	gcgtgatatt	ggtttggaaac	tggccgacac	1140
gttaagccgc	aacttatccg	ccaggcaatg	ggattaaacg	atttgcttga	1200
taa					1203

<210> 111

<211> 1179

<212> DNA

<213> E. Coli

<400> 111

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cggtaagtc	acggggcgct	ggccgtacat	ttgatttgc	cgactgcgc	120
gctcatccgg	gttttgcgtt	acgagcgata	gcgcgtggc	cggttacccgt	180
gcgcgcgtcg	gcgtctggca	atctctggc	gatttgcgc	ctgccccatc	240
gtcagcgatc	gtggtcacgc	tggatttgc	accctcgcc	cagaagatta	300
gcgcgtggac	agggttgcga	attgcacaat	gtcggcaac	ggctgtttgc	360
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ctcggtatgc	gagatgtat	gagtcttgc	gaaaccttga	ctcaggcgca	960
gaagacatgg	gggattacgg	cgtattgtgc	cgttatcagc	agcgtcgaca	1020
gaagcaacca	ttggcgtcac	ggacagccctt	gtacatctt	ttgccaacgg	1080
ctgggtgtcg	ggcgcaacat	cgggcgtatg	acgatggat	tattcacc	1140
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<210> 112

<211> 1326

<212> DNA

<213> E. Coli

<400> 112

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caacccggca	gcgcccgcgt	gattttgt	gcaccagaag	taacacgtag	cgccgacagc	120
gaataccccc	atcgtcagaa	cagtgactc	tggtaactca	ccggctttaa	cgaaccggaa	180
gcggtgtctgg	tgctgattaa	aagcgatgac	actcataacc	acagcgtttct	gtttaaccgc	240
gttcgcgacc	tgacggcgga	gatctggtt	ggccgtcgct	taggccagga	tgccgcgcca	300
gagaaaactgg	gcgttgaccg	cgcaactggca	ttcagcgaaa	tcaatcagca	actttatcaa	360
ctacttaacg	gcctgatgt	gtttaaccat	gcccaggcg	aatatgcata	tgctgatgta	420
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	caatga					1326

<210> 113

<211> 585

<212> DNA

<213> E. Coli

<400> 113

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ggcggttaacg	atgacagctc	atggcttacc	ctacttcacg	acctgacgaa	cgaaggcatg	180
gcttcggtc	atgagctggc	acaggcactg	cgtaaaaatgc	actctgcac	cagcgatgcc	240
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acgcaaccga	agctggataa	agtgaccggc	gaaaccgggt	aagctatcga	cgatctgcgt	420
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gaagagatca	tcgaatacgt	tcgtgttgc	gcccgttta	gccacgacac	ctttactcat	540
ccgcaaccga	ccgcgcccaga	agtacaaaaaa	ccgactctac	actaa		585

<210> 114

<211> 363

<212> DNA

<213> E. Coli

<400> 114

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gtggtttttgc	gtgtttgtat	ctatgtcg	catacaaacc	aagctcttgc	aaacttcgca	120
gttgcgttgc	tggctgttag	ctttagctt	ttcgcaat	caaaattcac	attcaaggca	180
tcgactacaa	cgatgcgcta	catgctat	gttgggttca	tggggacact	gagtgtact	240
gttggatggg	ctgctgtat	atgcgcactt	cccccgatga	taactcttgc	caccccttcc	300
gccatcagcc	tgggtgtcg	tttcgtctat	tcaaagttca	ttgtctttag	ggatgcgaaa	360
tga						363

<210> 115

<211> 921

<212> DNA

<213> E. Coli

<400> 115

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aaaacggtaac gtgaattcga agaattgaag tcatatgaag tggaaatcgt tttcataaaat 60
gacggcagca aagacgctac ggagtcaatc attaatgctc tggctgttgc agatcctcta 120
gttggccgc tgcattttac acgcaacttt ggttaaagaac cagcattgtt tgccagggtt 180
gaccatgcaa ccggggatgc gataatccca attgtatgttgc acctgcaaga cccgattgag 240
gttattcctc atcttattga aaaatggcaa gcaggtgctg atatggttct tgctaaaaga 300
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cacaataaaa taagcaatcc taaaattgaa gagaatgttgc gtgatttcag gctgtatgagc 420
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<211> 1332

<212> DNA

<213> E. Coli

<400> 116

<210> 117

<211> 249

<212> DNA

<213> E. Coli

<400> 117

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gtagtcggcg	gatggatcg	cacgctgtt	ggcttggta	aagtgcgtgg	cttcaatttt	180
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aaaagttaa						249

<210> 118
<211> 183
<212> DNA
<213> E. Coli

<400> 118

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gatctggtga	ataccgtacg	ttcttatgac	acggaaaacg	aacatgtatgt	ttgtgggttgg	180
taa						183

<210> 119
<211> 360
<212> DNA
<213> E. Coli

<400> 119

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<210> 120
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<212> DNA
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<400> 120

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<210> 121
<211> 1395
<212> DNA
<213> E. Coli

<400> 121

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<210> 122
 <211> 3123
 <212> DNA
 <213> E. Coli

<400> 122

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<211> 3078
<212> DNA
<213> E. Coli

<400> 123

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<211> 1416

<212> DNA

<213> E. Coli

<400> 124

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<211> 1035
<212> DNA
<213> E. Coli

<400> 125

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<210> 126
<211> 2481
<212> DNA
<213> E. Coli

<400> 126

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<211> 720

<212> DNA

<213> E. Coli

<400> 127

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<210> 128

<211> 543

<212> DNA

<213> E. Coli

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<210> 129

<211> 339			
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<400> 133

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1059

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<211> 621
<212> DNA
<213> E. Coli

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<211> 696
<212> DNA
<213> E. Coli

<400> 135

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<210> 136

<211> 636

<212> DNA

<213> E. Coli

<400> 136

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<210> 138

<211> 531

<212> DNA

<213> E. Coli

<400> 138

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<210> 139

<211> 1149

<212> DNA

<213> E. Coli

<400> 139

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<210> 140

<211> 417

<212> DNA

<213> E. Coli

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<213> E. Col

<400> 143

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<210> 145

<211> 291

<212> DNA

<213> E. Coli

<400> 145

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<210> 146

<211> 948

<212> DNA

<213> E. Coli

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<210> 147

<211> 891

<212> DNA

<213> E. Coli

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<210> 148

<211> 1668

<212> DNA

<213> E. Coli

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cgttggttcc	tcgaccgtat	cgccacgcac	attctggatt	accaggatga	agttaaagtt	1560
gagtcttcg	aaggtaactt	taccgagttc	gaagagtaca	agaaacgcac	gctggcgc	1620
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<210> 149
<211> 522
<212> DNA
<213> E. Coli

<400> 149

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acatgggtt ccctctatga aaaacatgaa gaaaaagggtt taattccaa acctaaaggc	180
gttagtgctg atccagagtt gcgttataag gtcgtaaag ctgtatcgac gcagcacatg	240
tcccttaatc aggctgtgc tcactttatg cttgtggta gtgggttgt agccagggtgg	300
ctgaagggtct atgaagagcg cggagaagct ggttacgca cgctcaagat tggcaccaaa	360
agaaacattt caatatcagt tgatccagaa aaagcggcat cagcatttga gctgtcaaaa	420
gaccgacgca ttgaggatct taaaaggcaaa gttcgatttc ttgaaacgca gcttatgtat	480
ctaaaaaaagc taaaaggcctt agctcatccc acgaaaaagt ga	522

<210> 150

<211> 852

<212> DNA

<213> E. Coli

<400> 150

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gcccacgtta aaaacgtat tagtgagatt ttcacgaga atagaggccg atacggatac	180
cgttaggtaa cgctgtctt tcatcgagaa gggaaacaga ttaaccataa agctgttcag	240
cgccctgatgg gaaccctctc acttaaagca gcgattaagg tcaagcgata ccgcctttac	300
agaggagagg tagggcaaac cggccctaat gttctccaa gagatttcaa ggctacgcgg	360
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gagcatcctg ttctgcactc tgaccaggaa tggcgttac gtatgagaag atatcaaaat	600
atccttaaag aacatggat taaaacaagc atgtccagaa aaggcaattt tctggataat	660
gctgtgggtgg agtgggttctt tggAACCTTA aagtccggat gttttatct tgatgagttc	720
agtaatataa gcaactgaa ggtgtgtt acggaatata ttgaaatacta caacagcaga	780
agaatttagcc taaaattttt aaggctgtact ccaatttgaat atcgaaatca gacctatatg	840
cctcggtttt aa	852

<210> 151

<211> 117

<212> DNA

<213> E. Coli

<400> 151

atgaaagttc gtgcttccgt caagaaattt tgccgttaact gcaaaatcgt taagcgtat	60
gggtgtcatcc gtgtgatttgc cagtgccgag ccgaacgata aacagcgcca aggctga	117

<210> 152

<211> 1332

<212> DNA

<213> E. Coli

<400> 152

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cgcagactgc tggttgcgtt cgggtgcgtt attgtgttcc gtattggctc ttttattccg	120

atccctggta	ttgatgccgc	tgtacttgcc	aaactgcttg	agcaacagcg	aggcaccatc	180
at gagatgt	ttaacatgtt	ctctggtgt	gctctcagcc	gtgcttcata	ctttgctctg	240
ggatcatgc	cgtatatttc	ggcgtcgatc	attatccagc	tgctgacggt	ggttcaccca	300
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cgttacggta	ctctgggtc	ggcaatattc	cagtcgatcg	gtattgtac	cggtctgccc	420
aatatgcctg	gtatgcaagg	cctgggtatt	aaccggct	ttgcattcta	cttcaccgct	480
gtttaagtgc	tggtcacagg	aaccatgttc	ctgatgtgg	tggcgaaca	gattactgaa	540
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caacgcgc	ttgtgtaaa	ctacgcgaaa	cgtcagcaag	gtcgtcggt	ctatgctgca	780
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ttcgggtggat	cctcactgct	tatcgttgg	gtcgtgatta	tggactttat	ggctcaagtg	1260
caaactctgat	tgtatgtcc	ttagtatgat	tctgcattgat	agaaggcgaa	cctgaaaggc	1320
tacggccgat	aa					1332

<210> 153

<211> 435

<212> DNA

<213> E. Coli

<400> 153

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cgttctggcg	gtggcgatcg	tgcgggtttc	gagggtggc	agatgcctct	gtaccgtcgt	180
ctgcccggaaat	tcggcgttac	ttctcgtaaa	gcagcgatta	cagccgaaat	tcgtctgtct	240
gacctggcta	aagttagaagg	cggtgttaga	gacctgaaca	cgctgaaagc	ggctaacatt	300
atcggtatcc	agatcgagtt	cgcgaaagtg	atcctggctg	gcaagtaac	gactccggta	360
actgttcgtg	gcctgcgtgt	tactaaaggc	gctcgtgtc	ctatcgaaac	tgctggcggt	420
aaaatcgagg	aataa					435

<210> 154

<211> 180

<212> DNA

<213> E. Coli

<400> 154

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aaggcaacgc	tgcttggcct	gggtctgcgt	cgtattggc	acaccgtaga	gcmcggaggat	120
actcctgcta	ttcgcgtat	gatcaacgc	gtttccttca	tggtaaagt	tgaggagtaa	180

<210> 155

<211> 504

<212> DNA

<213> E. Coli

<400> 155

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gtatctaaaa	ccgttaaagg	tggtcgtatt	ttctccttca	cagctctgac	tgttagttggc	120
gatggtaacg	gtcgcgttgg	ttttgggtac	ggtaaagcgc	gtgaagttcc	agcagcgtac	180
cagaaagcga	tggaaaaagc	ccgtcgcaat	atgatatacg	tcgcgtgaa	taacggcact	240

ctgcaacacc	ctgttaaagg	tgttcacacg	ggttctcg	tattcatgca	gccggcttcc	300
gaaggtaccc	gtatcatgc	cggtgg	atgcgc	ttctgga	cgctggg	360
cataacgttc	tggctaaagc	ctatgg	accaacc	tcaacgt	tcgt	420
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gttgaagaaa	ttctgg	aaata	at	aaatcc	tt	504
<210> 156						
<211> 354						
<212> DNA						
<213> E. Coli						
<400> 156						
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caactgaagt	acaccg	taa	caaagac	gctc	tggt	240
cgcgtctgg	aaaagg	cat	aaagat	tg	tg	300
ggtcgtgtcc	aggcact	ggc	agatg	ctg	cc	354
<210> 157						
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<212> DNA						
<213> E. Coli						
<400> 157						
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gttgaag	aacatgc	aga	taatacc	ac	act	180
ggtggg	aggctgg	tac	cgcgt	cg	gtat	240
gaaggctt	ctaaga	agct	gttact	caat	gttat	300
aatgtgat	acctgt	tct	gggtt	acc	gtc	360
atca	tttct	cat	ccgtt	accat	ca	420
atc	actgt	ct	tttct	cat	ccgtt	480
atc	actgt	ct	tttct	cat	ccgtt	534
<210> 158						
<211> 393						
<212> DNA						
<213> E. Coli						
<400> 158						
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aacaaagctg	cgg	tac	ccat	gc	ttc	120
aaggaagaag	gtt	tttatt	taa	ag	ttttaa	180
cttactctga	agt	attt	c	gg	aaag	240
ccagg	gtc	tata	aa	ac	ccaa	300
atc	cgat	tt	aa	gt	cc	360
cttgg	gg	tt	aa	gt	cc	393
<210> 159						
<211> 306						
<212> DNA						
<213> E. Coli						
<400> 159						
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ttcgc	gaaac	g	ac	ac	gc	120

cgttggAACG	ctgttctCAA	gctgcAGACT	ctGCCGCGTG	attccAGCCC	gtctcgTCAG	180
cgtAACCgCT	gccgtCAAAC	aggTCGTCCG	catggTTCC	tgcggAAAGTT	cgggttgAGC	240
cgtattaAGG	tccgtGAAGC	cgctatGCgc	ggtGAAATCC	cgggtctgAA	aaaggctAGC	300
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<210> 160

<211> 540

<212> DNA

<213> E. Coli

<400> 160

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aactacaATT	ctgtcatgCA	agtCCCTCGG	gtcgagaAGA	tcaccCTgAA	catgggtgTT	120
ggtaAGCgA	tcgctgACAA	aaaACTGCTG	gataAcGcAG	cagcagACCT	ggcagcaATC	180
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cagggtatC	cgatCggCTG	taaAGTAact	ctgcgtggCG	aacgcAtgtG	ggagttCTTT	300
gagcgcCTGA	tcactattGC	tgtacCTCGT	atccgtgACT	tccgtggCCT	gtccgctaAG	360
tcttcgACG	gtcgtggTA	ctacAGCATG	ggtgtCCGTG	agcagatCAT	cttcccAGAA	420
atcgactACG	ataAAAGTCGA	cccggttCGT	ggtttggATA	ttaccattAC	cactactGCg	480
aatctgACG	aagaaggCCG	cgctctgCTG	gctgcCTTtG	acttcccGTT	ccgcaagtaA	540

<210> 161

<211> 315

<212> DNA

<213> E. Coli

<400> 161

atggcagCgA	aaatCCGTCG	tgtgacgAA	gttatCgtGT	taaccGGTA	agataAAAGGT	60
aaacgcggTA	aagttaAGAA	tgtcctgtCT	tccggcaAGG	tcattgttGA	aggtatCAAC	120
ctgggttaAGA	aacatcAGAA	gccggTTCCG	gccctgAAcc	aaccgggtGG	catcgTTgAA	180
aaagaAGCCG	ctattcAGGT	ttccaACgTA	gcaatCTTC	atgcggCAC	cggcaaggCT	240
gaccgtgtAG	gctttagATT	cgaagacGGT	aaaaaaAGTCC	gtttcttCAA	gtctaACAGC	300
gaaactatCA	agtaA					315

<210> 162

<211> 372

<212> DNA

<213> E. Coli

<400> 162

atgatCCAAG	aacagactAT	gctgaACgTC	gccgacaACT	ccggTgCaCg	tcgcgtAATG	60
tgtatcaAGG	ttctgggtGG	ctcgCACCGT	cgctacgCAG	gcgtaggCgA	catcatCAAG	120
atcaccatCA	aagaAGCAAT	tccgcgtGGT	aaggTCAAA	aaggTgATGT	gctgaaggCG	180
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ggtatgtCTT	gtgttCTTCT	gaacaacaAC	agcgagCAGC	ctatcggtAC	gcgtatTTT	300
gggcccggTA	ctcgtgagCT	tcgttagtGAG	aagttcatGA	aaattatCTC	tctggcacCA	360
gaagtactCT	aa					372

<210> 163

<211> 567

<212> DNA

<213> E. Coli

<400> 163

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gtttatgCTG	ctgatgAAAG	ttctggcgAA	attcacttA	agggggAGGt	tattgaAGCA	120
ccttgtAAA	ttcatccAGA	agatattGAT	aaaaacatAG	atcttggACA	agtcacgACA	180

accatataa accgggagca tcatalogaat aaagtggccg tcgacattcg cttgatcaac	240
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ttcgatagca cggctaagac aactggtgct acgccttgc tgagcaacac cagtcaggc	360
gaagcaactg gggcgtgt acgactgatg gacaaaaatg acggtacat cgtattaggt	420
tcagccgcgc cagatctga cctggatgca agctcatcag aacagacgt gaacctttc	480
gcctggatgg aacaattga taatgcagtc gatgtcacgg caggtgaagt aaccgctaacc	540
gcaacctacg tgctggatta taaataa	567

<210> 164

<211> 1284

<212> DNA

<213> E. Coli

<400> 164

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ttcacctttg acccaggcct cacttcaacc gcacccctcg aatctaaaat tactttatt	180
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<210> 165

<211> 1434

<212> DNA

<213> E. Coli

<400> 165

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gttaaaatgtga ataccatcgaa agaacgtccg ggcggcgccg ctaacgtggc gatgaatatc	180
gcttctctcg gtgctaattgc acgcctggc ggggttgcgg gcatgttgc tgcacgcgc	240
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gccgggagta	aagaagtctg	ggccaacgg	ggcgaagtgt	tggtgctcaa	ctttgaagac	1380
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<210> 166

<211> 2841

<212> DNA

<213> E. Coli

<400> 166

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tttgcgcagg	acacgcgtat	tgcgcatcca	gagtggctga	cggaacttgg	aagccaaccc	180
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cgtcagggtc	tcgaccatct	gatgcgc	ctgctaagt	atgtctgtc	gcgtgaagac	1560
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<213> E. Coli

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<212> DNA

<213> E. Coli

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<211> 384

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<213> E. Coli

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tgcataaccgt	atcatgatta	a				4281

<210> 181
 <211> 369
 <212> DNA
 <213> E. Coli

<400> 181

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acagctgttt	acgggtctga	tgaaaacatt	attttatga	ggtatgtga	aaaattacat	120
ttagataaat	actctgttaa	aaatacggta	aaaactgaaa	caatggcgat	acaatttagct	180
gaaatataat	ttaggtatcg	ctatggcgaa	cggattgcag	aagaagaaaa	accatattta	240
attacggAAC	taccagatag	ttgggttgtt	gagggagcaa	agttaccta	tgaagttgcg	300
gggttgtat	ttattataga	aattaataag	aaaaatggat	gtgtttgaa	tttccatcat	360
agtaaataa						369

<210> 182

<211> 711
<212> DNA
<213> E. Coli

<400> 182

atgctggcgc tcatggatgc ggatggaaac attgcgtgga gcggggagta tgatgagtgg	60
ggcaaccagg tgaatgaaga gaacccgcat cacctgcacc agccgtaccg gctgccgggg	120
cagcagtatg ataaggagtc ggggctgtac tacaaccgga accggtaacta cgatccgttg	180
cagggcggt atatcactca ggacccgata gggctggagg gggatggag tctgtatgcg	240
tatccgctga atccggtaa tggatttatccataggta taagtccgc agatgttagcg	300
ctaataagaa gaaaagatca actaaaccat caaagagcat gggatattat atctgatact	360
tatgaagata tgaagagatt aaattttagt gggactgatc aatttttcca ttgtatggca	420
ttttgtcgag tgtctaaatt aaatgacgct ggttttagcc gatcggcgaa aggctgggt	480
tatgaaaaag agatttaga ttacgggtt aatctgttcg gtatgtacgg cagaaaagta	540
aagctatccc attctgaaat gattgaagat aataaaaaag acttggctgt aaatgaccat	600
gggttgacat gtccatcaac aacagattgc tcagatagat gtatgtatta tattaatcca	660
gagcataaaaaaa aaacgataaa ggctttacaa gatgtggct atctcaagta a	711

<210> 183

<211> 261

<212> DNA

<213> E. Coli

<400> 183

atgctggcta tctcaagtaa tctatcaaag atgataatat ttatTTTTC tattataatc	60
attgttgtt tatgcgtaat tacttatctt tatttataca aagatgaatc tcttgtaagt	120
aaacattaca taaactatataat ggcaatacca gaaaatgatg gagttttac atggctccca	180
gatTTTTTC cgcacgtac ggtggatata tcaatataca caaatgtaga agatgattat	240
ttttttctta tttttcccta a	261

<210> 184

<211> 192

<212> DNA

<213> E. Coli

<400> 184

gtgagggcca gggacaagt ggcggaaatc gtatcaaaga atgatccaga tacaaaaaaaaa	60
gtgtgtgtaa aatatggtaa gataccaggc caagggatg gtgtaaacct ttTTTTGTT	120
ggtgaaattaa atgttacgca ttatTTATA acaaataattg gagctggatt gcctgatgct	180
tgtgcagagt aa	192

<210> 185

<211> 504

<212> DNA

<213> E. Coli

<400> 185

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aaactcaggc cgccagtcgtt aacctcgcgc atacagccgg gcagtgcgtt catcgctgc	120
gcggaaatgg acgaacagtg gggctatgtc gggcttaat cgccgcagcg ctggctgttt	180
tacgcgtatg acagtctccg gaagacgggtt gttgcgcacg tattcggtga acgcactatg	240
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gatggctggc cgctgtatga atcccgctg aaggaaagc tgccacgtaat cagcaagcga	360
tatacgcagc gaattgagcg gcataacctg aatctgaggc agcacctggc acggctggga	420
cggaaagtgcg tgcgttctc aaaatcggtg gagctgcattt acaaagtcat cggcattat	480
ctgaacataa aacactatca ataa	504

<210> 186
<211> 276
<212> DNA
<213> E. Coli

<400> 186

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ggcaaaaagca ccgcggaca tcagcgctat ctctgctctc actgccgtaa aacatggcaa	120
ctgcagttca cttacaccgc ttctcaaccc ggtacgcacc agaaaatcat tgatatggcc	180
atgaatggcg ttggatgccg ggcaacagcc cgccattatgg gcgttggcct caacacgatt	240
ttacgtcact taaaaaactc aggccgcagt cggtaa	276

<210> 187

<211> 417
<212> DNA
<213> E. Coli

<400> 187

atgatgacta aaacccaaat aaataaattt ataaaaatga tgaatgattt agactatcca	60
tttgaagcac cgctcaagga atcattttt gaaagtataa tccaaataga atttaattct	120
aattcaacta attgccttga gaagttatgt aatgaagttt gtattcttt taagaatcaa	180
cctgatttac ttactttttt aagagcaatg gatggattcg aagttaatgg attacgatta	240
tttagcctct cgattccaga accttcagg taaaaacctt ttgcccgtaaa tgaattttat	300
agaaaataatg atgatttcat aaaccctgtt ctacaagaac ggttagtgat cggggatttat	360
agcatttcaa tatttactta tgacattaaa ggtgatgctg ccaacttact gatttag	417

<210> 188

<211> 1179
<212> DNA
<213> E. Coli

<400> 188

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tgtggactt ctgagtcac aggtatcg tggcagagcg ggcattggaa tgaaatattt	120
acattctcac tcttaataaa tattaataat acggggcttg gttcacagtt ccatggata	180
acattttgtt aattaatttga taaaagcact ccattatttta ttaattccat taacaataat	240
gaacaattat ttatggatt tgacttctat cgaataaaata gatttggtag attggaaaag	300
tattattata tacaactaag aggccctttt ttatcggcta ttcacacca gatcattgaa	360
aaccaactgg atacagaaac aataactatt agttatgaat ttatcctctg tcaacatctt	420
atcgcaaata ccgagttcag ctatggca ctccctgaaa attataaccg tttgtttta	480
ccaaattcaa aaaacccaaac aaataatcg ttcaaaaacgt taaacagcaa agctattggc	540
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gaaaaactgg gtggagatgc aataaaaggc tatgtcaaa tactaaatga aaaaacagcg	660
ggcatagcga tagcaacagc atctattctt ttaacaaagc gttctaattt tgatacatat	720
acagaaataa atagttactt aggcaactt agaggtcaac aaaaacttct tgatggata	780
gacataatag aaataatata cattaagaga ccttcaaaag acttagctaa cttacgaaag	840
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tcttggaaat tcaacgcccga agaccttttta agaatgagaa agggcaatgt tcctctaaat	960
tataatgttc accataaact atctcttagat gatgggttta ctaatgattt cgaaaattta	1020
gttataatcg aaaacgaacc atatcataaa gttttacta acatgcaatc acgaatagct	1080
aagggaatat tagtaggtga aagcaaaatc actccctggg ccattccatc tggctcaatt	1140
tatcctccca tgaaaaatata tatggaccac acaaaatga	1179

<210> 189

<211> 666
<212> DNA
<213> E. Coli

<400> 189

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aaacctcata	cgatccctc	tagatatctt	tgcgagtata	ttagaagcat	tgagaaaaat	120
ggccacgccc	ttgattttgg	ctgcggaaaa	cttagatatt	ctgatgaatt	aatcagtaaa	180
tttgatgaag	ttactttct	agactcgaaa	aggcaacttg	aaagagagca	aattattaga	240
ggaattaaaa	ctaaaattat	tgactatgtc	ccacgatatt	ataaaaatgc	aaatacagtt	300
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ctctctgccg	ttccttgtcg	ggataacaatc	gacaaaatag	ttcttagcat	caagagatta	420
ctaaaatcat	gagggtgagac	tcttattgtt	aatcaatata	aaagctcata	cttcaaaaaaa	480
tacgaaacag	gaagaaaaaca	tcttacgta	tacattaca	aaaattcaaa	aagtgtttct	540
tactatggat	tactcgatga	actcgacgtg	caagaaaat	gttcttcaca	tggccttgaa	600
atattaaagt	cgtggagtaa	agcaggaagt	tcatatgtca	ctgttggag	ttgtaatgca	660
atataa						666

<210> 190

<211> 705

<212> DNA

<213> E. Coli

<400> 190

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ttaataacat	taccaaccaa	gtatgtccca	cctattaaag	atcatgagag	ctttattaaat	180
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ggtgcgttag	acctacataa	caatgcagcc	aaactacttc	gggtgcgata	tctttggat	300
aagcatctaa	ttataaaaacc	gttattcacgg	agagctggag	tcaacagaaa	attaaataaa	360
gatgaagctc	acaatgtaat	gagcaatcta	tattaccctg	aagtaagaaa	aattgaagac	420
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tcgataattt	cattaatttc	cttcctaata	atctttttt	gcaaacaaat	ggatattttt	540
catgttgaag	gttcttgct	gtctttatcc	ttttttgtaa	ttttatcatt	ctcagtgagt	600
ggtattatct	ttgctttgac	agttaaagccc	agaactgaaa	gtcaagtccg	aaaaatcccc	660
gacgataaaaa	taaaagaatt	tttcactaaa	aataacatta	attga		705

<210> 191

<211> 285

<212> DNA

<213> E. Coli

<400> 191

atgtttacta	tcaacgcaga	agtacgtaaa	gagcagggtt	agggtgcgag	ccggccgcctg	60
cgtgccgcta	acaagttccc	gcgaatcatc	tacgtggca	aagaagcgcc	gctggctatc	120
gagctggatc	acgacaaagt	catgaacatg	caagctaaag	ctgaattcta	cagcgaagtt	180
ctgaccatcg	ttgttgcacgg	taaagaaatc	aaagttaaag	ctcaggacgt	acagcgtcac	240
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<210> 192

<211> 1977

<212> DNA

<213> E. Coli

<400> 192

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cgtgaagagg	ccatccacgc	gttgaactcaa	cgtcttgctg	ctctggggaa	aatttccagt	180
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gcccacactca	gcgagccgct	tcagtggaa	ggcgttgatg	gccccggaagc	agttgattta	360
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ttggcggcgtc	acgcqgttaa	qcatqqcaac	tatctqactq	atqqcqtaat	qccataaa	1977

<210> 193
<211> 2634
<212> DNA
<213> E. Col

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gccccaaaaaa gtgacgctga agggatactg gaaaatgctt tctggcaaat tgcgctcaat	1500
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cgtattgatg tggatataaa tcttgataaac caggctgacg atcatcgct tcgtgtcctg	1860
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<210> 194
 <211> 1572
 <212> DNA
 <213> E. Coli

<400> 194

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 <212> DNA
 <213> E. Coli

<400> 195

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<210> 196

<211> 1371

<212> DNA

<213> E. Coli

<400> 196

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<211> 186
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 <213> E. Coli

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 tactaa 186

<210> 198
 <211> 93
 <212> DNA
 <213> E. Coli

<400> 198
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<210> 199
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 <212> DNA
 <213> E. Coli

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 <212> DNA
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 gggcatcgaa atattcgcca tactgtgcgt tataccgcca gtaatgctgc tcgtttgcc 540
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<210> 201
 <211> 549
 <212> DNA

<213> E. Coli

<400> 201

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tttagtttag	aaacaaccct	gaataacgaa	accaatacca	ttccgttcca	ggcgcttat	480
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<210> 202

<211> 648

<212> DNA

<213> E. Coli

<400> 202

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<210> 203

<211> 726

<212> DNA

<213> E. Coli

<400> 203

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<210> 204

<211> 2637

<212> DNA

<213> E. Coli

<400> 204

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<210> 205

<211> 531

<212> DNA

<213> E. Coli

<400> 205

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<211> 534

<212> DNA

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<400> 209

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<211> 312

<212> DNA

<213> E. Coli

<400> 210

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<210> 211

<211> 291

<212> DNA

<213> E. Coli

<400> 211

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<211> 1119

<212> DNA

<213> E. Coli

<400> 215

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<210> 216

<211> 591

<212> DNA

<213> E. Coli

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<210> 217

<211> 993

<212> DNA

<213> E. Coli

<400> 217

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<210> 218
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<212> DNA
<213> E. Col.

<400> 218

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<210> 219
<211> 1104
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<400> 219

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aaggttaaaa	ctcaaata	ttgacgggg	ccgcacaag	cggtggagca	tgtgtttaa	960
ttcgatgca	cgcgaagaac	cttacctgg	ttgacatcc	acggaaagt	tcagagatga	1020
aatgtgcct	tcgggaaccg	tgagacaggt	gctgcac	tgtcgta	tcgtgttgc	1080
aatatgttggg	ttaagtcccg	caacgagcgc	aacccttac	cttgcgttgc	agcggccgg	1140
ccgggaactc	aaaggagact	gccagtata	aactggagga	aggtgggat	gacgtcaagt	1200

catcatggcc	cttacgacca	gggctacaca	cgtgctacaa	tggcgcatac	aaagagaagc	1260
gacctcgca	gagcaagcgg	acctcataaa	gtgcgtcgta	gtccggattt	gagtctgcaa	1320
ctcgactcca	tgaagtcgga	atcgcttagta	atcggttgcac	agaatgccac	ggtgaatacg	1380
ttccccggcc	ttgtacacac	cgcgggtcac	accatgggag	tgggttgc当地	aagaagttagg	1440
tagcttaacc	ttcgggagggg	cgcttaccac	tttgtgattc	atgactgggg	tgaagtgc当地	1500
acaaggtaac	cgtagggaa	cctgcgggtt	gatcacctcc	ttaccttaa		1549

<210> 243

<211> 221
<212> PRT
<213> E. Coli

<400> 243

Met	Asn	Val	Phe	Ser	Gln	Thr	Gln	Arg	Tyr	Lys	Ala	Leu	Phe	Trp	Leu
1			5					10							15
Ser	Leu	Phe	His	Leu	Leu	Val	Ile	Thr	Ser	Ser	Asn	Tyr	Leu	Val	Gln
							20		25						30
Leu	Pro	Val	Ser	Ile	Leu	Gly	Phe	His	Thr	Thr	Trp	Gly	Ala	Phe	Ser
							35		40						45
Phe	Pro	Phe	Ile	Phe	Leu	Ala	Thr	Asp	Leu	Thr	Val	Arg	Ile	Phe	Gly
							50		55						60
Ala	Pro	Leu	Ala	Arg	Arg	Ile	Ile	Phe	Ala	Val	Met	Ile	Pro	Ala	Leu
65							70			75					80
Leu	Ile	Ser	Tyr	Val	Ile	Ser	Ser	Leu	Phe	Tyr	Met	Gly	Ser	Trp	Gln
							85			90					95
Gly	Phe	Gly	Ala	Leu	Ala	His	Phe	Asn	Leu	Phe	Val	Ala	Arg	Ile	Ala
							100			105					110
Thr	Ala	Ser	Phe	Met	Ala	Tyr	Ala	Leu	Gly	Gln	Ile	Leu	Asp	Val	His
							115		120						125
Val	Phe	Asn	Arg	Leu	Arg	Gln	Ser	Arg	Arg	Trp	Trp	Leu	Ala	Pro	Thr
							130		135						140
Ala	Ser	Thr	Leu	Phe	Gly	Asn	Val	Ser	Asp	Thr	Leu	Ala	Phe	Phe	Phe
145							145		150						160
Ile	Ala	Phe	Trp	Arg	Ser	Pro	Asp	Ala	Phe	Met	Ala	Glu	His	Trp	Met
							165			170					175
Glu	Ile	Ala	Leu	Val	Asp	Tyr	Cys	Phe	Lys	Val	Leu	Ile	Ser	Ile	Val
							180		185						190
Phe	Phe	Leu	Pro	Met	Tyr	Gly	Val	Leu	Leu	Asn	Met	Leu	Leu	Lys	Arg
							195		200						205
Leu	Ala	Asp	Lys	Ser	Glu	Ile	Asn	Ala	Leu	Gln	Ala	Ser			
							210		215						220

<210> 244

<211> 203

<212> PRT

<213> E. Coli

<400> 244

Met	Ile	Arg	Trp	Met	Asn	Glu	Pro	Leu	Trp	Pro	Phe	Ile	Glu	Arg	Lys
1							5			10					15
Lys	Ser	Met	Arg	Asn	Leu	Val	Lys	Tyr	Val	Gly	Ile	Gly	Leu	Leu	Val
							20			25					30
Met	Gly	Leu	Ala	Ala	Cys	Asp	Asp	Lys	Asp	Thr	Asn	Ala	Thr	Ala	Gln
							35			40					45
Gly	Ser	Val	Ala	Glu	Ser	Asn	Ala	Thr	Gly	Asn	Pro	Val	Asn	Leu	Leu

50	55	60													
Asp	Gly	Lys	Leu	Ser	Phe	Ser	Leu	Pro	Ala	Asp	Met	Thr	Asp	Gln	Ser
65					70						75				80
Gly	Lys	Leu	Gly	Thr	Gln	Ala	Asn	Asn	Met	His	Val	Trp	Ser	Asp	Ala
					85					90				95	
Thr	Gly	Gln	Lys	Ala	Val	Ile	Val	Ile	Met	Gly	Asp	Asp	Pro	Lys	Glu
					100			105					110		
Asp	Leu	Ala	Val	Leu	Ala	Lys	Arg	Leu	Glu	Asp	Gln	Gln	Arg	Ser	Arg
	115					120					125				
Asp	Pro	Gln	Leu	Gln	Val	Val	Thr	Asn	Lys	Ala	Ile	Glu	Leu	Lys	Gly
	130					135					140				
His	Lys	Met	Gln	Gln	Leu	Asp	Ser	Ile	Ile	Ser	Ala	Lys	Gly	Gln	Thr
145					150					155				160	
Ala	Tyr	Ser	Ser	Val	Ile	Leu	Gly	Asn	Val	Gly	Asn	Gln	Leu	Leu	Thr
					165				170				175		
Met	Gln	Ile	Thr	Leu	Pro	Ala	Asp	Asp	Gln	Gln	Lys	Ala	Gln	Thr	Thr
					180			185					190		
Ala	Glu	Asn	Ile	Ile	Asn	Thr	Leu	Val	Ile	Gln					
					195			200							

<210> 245

<211> 324

<212> PRT

<213> E. Coli

<400> 245

Met	Ala	Asn	Met	Phe	Ala	Leu	Ile	Leu	Val	Ile	Ala	Thr	Leu	Val	Thr
1				5					10				15		
Gly	Ile	Leu	Trp	Cys	Val	Asp	Lys	Phe	Phe	Phe	Ala	Pro	Lys	Arg	Arg
				20				25					30		
Glu	Arg	Gln	Ala	Ala	Ala	Gln	Ala	Ala	Ala	Gly	Asp	Ser	Leu	Asp	Lys
				35				40			45				
Ala	Thr	Leu	Lys	Lys	Val	Ala	Pro	Lys	Pro	Gly	Trp	Leu	Glu	Thr	Gly
				50				55			60				
Ala	Ser	Val	Phe	Pro	Val	Leu	Ala	Ile	Val	Leu	Ile	Val	Arg	Ser	Phe
	65				70				75				80		
Ile	Tyr	Glu	Pro	Phe	Gln	Ile	Pro	Ser	Gly	Ser	Met	Met	Pro	Thr	Leu
				85				90				95			
Leu	Ile	Gly	Asp	Phe	Ile	Leu	Val	Glu	Lys	Phe	Ala	Tyr	Gly	Ile	Lys
				100				105				110			
Asp	Pro	Ile	Tyr	Gln	Lys	Thr	Leu	Ile	Glu	Thr	Gly	His	Pro	Lys	Arg
		115				120				125					
Gly	Asp	Ile	Val	Val	Phe	Lys	Tyr	Pro	Glu	Asp	Pro	Lys	Leu	Asp	Tyr
		130				135				140					
Ile	Lys	Arg	Ala	Val	Gly	Leu	Pro	Gly	Asp	Lys	Val	Thr	Tyr	Asp	Pro
145				150				155				160			
Val	Ser	Lys	Glu	Leu	Thr	Ile	Gln	Pro	Gly	Cys	Ser	Ser	Gly	Gln	Ala
				165				170			175				
Cys	Glu	Asn	Ala	Leu	Pro	Val	Thr	Tyr	Ser	Asn	Val	Glu	Pro	Ser	Asp
				180				185			190				
Phe	Val	Gln	Thr	Phe	Ser	Arg	Arg	Asn	Gly	Gly	Glu	Ala	Thr	Ser	Gly
		195				200					205				
Phe	Phe	Glu	Val	Pro	Lys	Asn	Glu	Thr	Lys	Glu	Asn	Gly	Ile	Arg	Leu
		210				215					220				
Ser	Glu	Arg	Lys	Glu	Thr	Leu	Gly	Asp	Val	Thr	His	Arg	Ile	Leu	Thr
225					230				235			240			

Val	Pro	Ile	Ala	Gln	Asp	Gln	Val	Gly	Met	Tyr	Tyr	Gln	Gln	Pro	Gly
				245					250					255	
Gln	Gln	Leu	Ala	Thr	Trp	Ile	Val	Pro	Pro	Gly	Gln	Tyr	Phe	Met	Met
				260				265				270			
Gly	Asp	Asn	Arg	Asp	Asn	Ser	Ala	Asp	Ser	Arg	Tyr	Trp	Gly	Phe	Val
				275				280			285				
Pro	Glu	Ala	Asn	Leu	Val	Gly	Arg	Ala	Thr	Ala	Ile	Trp	Met	Ser	Phe
				290			295				300				
Asp	Lys	Gln	Glu	Gly	Glu	Trp	Pro	Thr	Gly	Leu	Arg	Leu	Ser	Arg	Ile
				305			310			315			320		
Gly	Gly	Ile	His												

<210> 246
 <211> 586
 <212> PRT
 <213> E. Coli

	<400>	246													
Met	Thr	Ile	Thr	Lys	Leu	Ala	Trp	Arg	Asp	Leu	Val	Pro	Asp	Thr	Asp
1				5				10					15		
Ser	Tyr	Gln	Glu	Ile	Phe	Ala	Gln	Pro	His	Leu	Ile	Asp	Glu	Asn	Asp
				20				25					30		
Pro	Leu	Phe	Ser	Asp	Thr	Gln	Pro	Arg	Leu	Gln	Phe	Ala	Leu	Glu	Gln
				35				40				45			
Leu	Leu	His	Thr	Arg	Ala	Ser	Ser	Ser	Phe	Met	Leu	Ala	Lys	Ala	Pro
				50				55			60				
Glu	Glu	Ser	Glu	Tyr	Leu	Asn	Leu	Ile	Ala	Asn	Ala	Ala	Arg	Thr	Leu
				65				70			75		80		
Gln	Ser	Asp	Ala	Gly	Gln	Leu	Val	Gly	Gly	His	Tyr	Glu	Val	Ser	Gly
				85				90					95		
His	Ser	Ile	Arg	Leu	Arg	His	Ala	Val	Ser	Ala	Asp	Asp	Asn	Phe	Ala
				100				105					110		
Thr	Leu	Thr	Gln	Val	Val	Ala	Ala	Asp	Trp	Val	Glu	Ala	Glu	Gln	Leu
				115				120				125			
Phe	Gly	Cys	Leu	Arg	Gln	Phe	Asn	Gly	Asp	Ile	Thr	Leu	Gln	Pro	Gly
				130				135			140				
Leu	Val	His	Gln	Ala	Asn	Gly	Gly	Ile	Leu	Ile	Ile	Ser	Leu	Arg	Thr
				145				150			155		160		
Leu	Leu	Ala	Gln	Pro	Leu	Leu	Trp	Met	Arg	Leu	Lys	Asn	Ile	Val	Asn
				165				170					175		
Arg	Glu	Arg	Phe	Asp	Trp	Val	Ala	Phe	Asp	Glu	Ser	Arg	Pro	Leu	Pro
				180				185				190			
Val	Ser	Val	Pro	Ser	Met	Pro	Leu	Lys	Leu	Lys	Val	Ile	Leu	Val	Gly
				195				200			205				
Glu	Arg	Glu	Ser	Leu	Ala	Asp	Phe	Gln	Glu	Met	Glu	Pro	Glu	Leu	Ser
				210				215			220				
Glu	Gln	Ala	Ile	Tyr	Ser	Glu	Phe	Glu	Asp	Thr	Leu	Gln	Ile	Val	Asp
				225				230			235		240		
Ala	Glu	Ser	Val	Thr	Gln	Trp	Cys	Arg	Trp	Val	Thr	Phe	Thr	Ala	Arg
				245				250				255			
His	Asn	His	Leu	Pro	Ala	Pro	Gly	Ala	Asp	Ala	Trp	Pro	Ile	Leu	Ile
				260				265			270				
Arg	Glu	Ala	Ala	Arg	Tyr	Thr	Gly	Glu	Gln	Glu	Thr	Leu	Pro	Leu	Ser
				275				280			285				

Pro Gln Trp Ile Leu Arg Gln Cys Lys Glu Val Ala Ser Leu Cys Asp
 290 295 300
 Gly Asp Thr Phe Ser Gly Glu Gln Leu Asn Leu Met Leu Gln Gln Arg
 305 310 315 320
 Glu Trp Arg Glu Gly Phe Leu Ala Glu Arg Met Gln Asp Glu Ile Leu
 325 330 335
 Gln Glu Gln Ile Leu Ile Glu Thr Glu Gly Glu Arg Ile Gly Gln Ile
 340 345 350
 Asn Ala Leu Ser Val Ile Glu Phe Pro Gly His Pro Arg Ala Phe Gly
 355 360 365
 Glu Pro Ser Arg Ile Ser Cys Val Val His Ile Gly Asp Gly Glu Phe
 370 375 380
 Thr Asp Ile Glu Arg Lys Ala Glu Leu Gly Gly Asn Ile His Ala Lys
 385 390 395 400
 Gly Met Met Ile Met Gln Ala Phe Leu Met Ser Glu Leu Gln Leu Glu
 405 410 415
 Gln Gln Ile Pro Phe Ser Ala Ser Leu Thr Phe Glu Gln Ser Tyr Ser
 420 425 430
 Glu Val Asp Gly Asp Ser Ala Ser Met Ala Glu Leu Cys Ala Leu Ile
 435 440 445
 Ser Ala Leu Ala Asp Val Pro Val Asn Gln Ser Ile Ala Ile Thr Gly
 450 455 460
 Ser Val Asp Gln Phe Gly Arg Ala Gln Pro Val Gly Gly Leu Asn Glu
 465 470 475 480
 Lys Ile Glu Gly Phe Phe Ala Ile Cys Gln Gln Arg Glu Leu Thr Gly
 485 490 495
 Lys Gln Gly Val Ile Ile Pro Thr Ala Asn Val Arg His Leu Ser Leu
 500 505 510
 His Ser Glu Leu Val Lys Ala Val Glu Glu Gly Lys Phe Thr Ile Trp
 515 520 525
 Ala Val Asp Asp Val Thr Asp Ala Leu Pro Leu Leu Leu Asn Leu Val
 530 535 540
 Trp Asp Gly Glu Gly Gln Thr Thr Leu Met Gln Thr Ile Gln Glu Arg
 545 550 555 560
 Ile Ala Gln Ala Ser Gln Gln Glu Gly Arg His Arg Phe Pro Trp Pro
 565 570 575
 Leu Arg Trp Leu Asn Trp Phe Ile Pro Asn
 580 585

<210> 247
 <211> 394
 <212> PRT
 <213> E. Coli

<400> 247

Met Ser Lys Glu Lys Phe Glu Arg Thr Lys Pro His Val Asn Val Gly
 1 5 10 15
 Thr Ile Gly His Val Asp His Gly Lys Thr Thr Leu Thr Ala Ala Ile
 20 25 30
 Thr Thr Val Leu Ala Lys Thr Tyr Gly Gly Ala Ala Arg Ala Phe Asp
 35 40 45
 Gln Ile Asp Asn Ala Pro Glu Glu Lys Ala Arg Gly Ile Thr Ile Asn
 50 55 60
 Thr Ser His Val Glu Tyr Asp Thr Pro Thr Arg His Tyr Ala His Val
 65 70 75 80
 Asp Cys Pro Gly His Ala Asp Tyr Val Lys Asn Met Ile Thr Gly Ala

85	90	95
Ala Gln Met Asp Gly Ala Ile Leu Val Val Ala Ala Thr Asp Gly Pro		
100	105	110
Met Pro Gln Thr Arg Glu His Ile Leu Leu Gly Arg Gln Val Gly Val		
115	120	125
Pro Tyr Ile Ile Val Phe Leu Asn Lys Cys Asp Met Val Asp Asp Glu		
130	135	140
Glu Leu Leu Glu Leu Val Glu Met Glu Val Arg Glu Leu Leu Ser Gln		
145	150	155
Tyr Asp Phe Pro Gly Asp Asp Thr Pro Ile Val Arg Gly Ser Ala Leu		
165	170	175
Lys Ala Leu Glu Gly Asp Ala Glu Trp Glu Ala Lys Ile Leu Glu Leu		
180	185	190
Ala Gly Phe Leu Asp Ser Tyr Ile Pro Glu Pro Glu Arg Ala Ile Asp		
195	200	205
Lys Pro Phe Leu Leu Pro Ile Glu Asp Val Phe Ser Ile Ser Gly Arg		
210	215	220
Gly Thr Val Val Thr Gly Arg Val Glu Arg Gly Ile Ile Lys Val Gly		
225	230	235
Glu Glu Val Glu Ile Val Gly Ile Lys Glu Thr Gln Lys Ser Thr Cys		
245	250	255
Thr Gly Val Glu Met Phe Arg Lys Leu Leu Asp Glu Gly Arg Ala Gly		
260	265	270
Glu Asn Val Gly Val Leu Leu Arg Gly Ile Lys Arg Glu Glu Ile Glu		
275	280	285
Arg Gly Gln Val Leu Ala Lys Pro Gly Thr Ile Lys Pro His Thr Lys		
290	295	300
Phe Glu Ser Glu Val Tyr Ile Leu Ser Lys Asp Glu Gly Arg His		
305	310	315
Thr Pro Phe Phe Lys Gly Tyr Arg Pro Gln Phe Tyr Phe Arg Thr Thr		
325	330	335
Asp Val Thr Gly Thr Ile Glu Leu Pro Glu Gly Val Glu Met Val Met		
340	345	350
Pro Gly Asp Asn Ile Lys Met Val Val Thr Leu Ile His Pro Ile Ala		
355	360	365
Met Asp Asp Gly Leu Arg Phe Ala Ile Arg Glu Gly Gly Arg Thr Val		
370	375	380
Gly Ala Gly Val Val Ala Lys Val Leu Gly		
385	390	

<210> 248
 <211> 704
 <212> PRT
 <213> E. Coli

<400> 248

Met Ala Arg Thr Thr Pro Ile Ala Arg Tyr Arg Asn Ile Gly Ile Ser		
1	5	10
Ala His Ile Asp Ala Gly Lys Thr Thr Thr Glu Arg Ile Leu Phe		
20	25	30
Tyr Thr Gly Val Asn His Lys Ile Gly Glu Val His Asp Gly Ala Ala		
35	40	45
Thr Met Asp Trp Met Glu Gln Glu Gln Glu Arg Gly Ile Thr Ile Thr		
50	55	60
Ser Ala Ala Thr Thr Ala Phe Trp Ser Gly Met Ala Lys Gln Tyr Glu		

65	70	75	80
Pro His Arg Ile Asn Ile Ile Asp Thr Pro Gly His Val Asp Phe Thr			
85	90	95	
Ile Glu Val Glu Arg Ser Met Arg Val Leu Asp Gly Ala Val Met Val			
100	105	110	
Tyr Cys Ala Val Gly Gly Val Gln Pro Gln Ser Glu Thr Val Trp Arg			
115	120	125	
Gln Ala Asn Lys Tyr Lys Val Pro Arg Ile Ala Phe Val Asn Lys Met			
130	135	140	
Asp Arg Met Gly Ala Asn Phe Leu Lys Val Val Asn Gln Ile Lys Thr			
145	150	155	160
Arg Leu Gly Ala Asn Pro Val Pro Leu Gln Leu Ala Ile Gly Ala Glu			
165	170	175	
Glu His Phe Thr Gly Val Val Asp Leu Val Lys Met Lys Ala Ile Asn			
180	185	190	
Trp Asn Asp Ala Asp Gln Gly Val Thr Phe Glu Tyr Glu Asp Ile Pro			
195	200	205	
Ala Asp Met Val Glu Leu Ala Asn Glu Trp His Gln Asn Leu Ile Glu			
210	215	220	
Ser Ala Ala Glu Ala Ser Glu Glu Leu Met Glu Lys Tyr Leu Gly Gly			
225	230	235	240
Glu Glu Leu Thr Glu Ala Glu Ile Lys Gly Ala Leu Arg Gln Arg Val			
245	250	255	
Leu Asn Asn Glu Ile Ile Leu Val Thr Cys Gly Ser Ala Phe Lys Asn			
260	265	270	
Lys Gly Val Gln Ala Met Leu Asp Ala Val Ile Asp Tyr Leu Pro Ser			
275	280	285	
Pro Val Asp Val Pro Ala Ile Asn Gly Ile Leu Asp Asp Gly Lys Asp			
290	295	300	
Thr Pro Ala Glu Arg His Ala Ser Asp Asp Glu Pro Phe Ser Ala Leu			
305	310	315	320
Ala Phe Lys Ile Ala Thr Asp Pro Phe Val Gly Asn Leu Thr Phe Phe			
325	330	335	
Arg Val Tyr Ser Gly Val Val Asn Ser Gly Asp Thr Val Leu Asn Ser			
340	345	350	
Val Lys Ala Ala Arg Glu Arg Phe Gly Arg Ile Val Gln Met His Ala			
355	360	365	
Asn Lys Arg Glu Glu Ile Lys Glu Val Arg Ala Gly Asp Ile Ala Ala			
370	375	380	
Ala Ile Gly Leu Lys Asp Val Thr Thr Gly Asp Thr Leu Cys Asp Pro			
385	390	395	400
Asp Ala Pro Ile Ile Leu Glu Arg Met Glu Phe Pro Glu Pro Val Ile			
405	410	415	
Ser Ile Ala Val Glu Pro Lys Thr Lys Ala Asp Gln Glu Lys Met Gly			
420	425	430	
Leu Ala Leu Gly Arg Leu Ala Lys Glu Asp Pro Ser Phe Arg Val Trp			
435	440	445	
Thr Asp Glu Glu Ser Asn Gln Thr Ile Ile Ala Gly Met Gly Glu Leu			
450	455	460	
His Leu Asp Ile Ile Val Asp Arg Met Lys Arg Glu Phe Asn Val Glu			
465	470	475	480
Ala Asn Val Gly Lys Pro Gln Val Ala Tyr Arg Glu Thr Ile Arg Gln			
485	490	495	
Lys Val Thr Asp Val Glu Gly Lys His Ala Lys Gln Ser Gly Gly Arg			
500	505	510	
Gly Gln Tyr Gly His Val Val Ile Asp Met Tyr Pro Leu Glu Pro Gly			
515	520	525	

Ser	Asn	Pro	Lys	Gly	Tyr	Glu	Phe	Ile	Asn	Asp	Ile	Lys	Gly	Gly	Val
530				535							540				
Ile	Pro	Gly	Glu	Tyr	Ile	Pro	Ala	Val	Asp	Lys	Gly	Ile	Gln	Glu	Gln
545				550						555				560	
Leu	Lys	Ala	Gly	Pro	Leu	Ala	Gly	Tyr	Pro	Val	Val	Asp	Met	Gly	Ile
				565					570				575		
Arg	Leu	His	Phe	Gly	Ser	Tyr	His	Asp	Val	Asp	Ser	Ser	Glu	Leu	Ala
				580				585				590			
Phe	Lys	Leu	Ala	Ala	Ser	Ile	Ala	Phe	Lys	Glu	Gly	Phe	Lys	Lys	Ala
				595				600			605				
Lys	Pro	Val	Leu	Leu	Glu	Pro	Ile	Met	Lys	Val	Glu	Val	Glu	Thr	Pro
				610				615			620				
Glu	Glu	Asn	Thr	Gly	Asp	Val	Ile	Gly	Asp	Leu	Ser	Arg	Arg	Arg	Gly
				625				630			635			640	
Met	Leu	Lys	Gly	Gln	Glu	Ser	Glu	Val	Thr	Gly	Val	Lys	Ile	His	Ala
				645				650			655				
Glu	Val	Pro	Leu	Ser	Glu	Met	Phe	Gly	Tyr	Ala	Thr	Gln	Leu	Arg	Ser
				660				665			670				
Leu	Thr	Lys	Gly	Arg	Ala	Ser	Tyr	Thr	Met	Glu	Phe	Leu	Lys	Tyr	Asp
				675				680			685				
Glu	Ala	Pro	Ser	Asn	Val	Ala	Gln	Ala	Val	Ile	Glu	Ala	Arg	Gly	Lys
				690				695			700				

<210> 249
<211> 179
<212> PRT
<213> E. Coli

<400> 249															
Met	Pro	Arg	Arg	Arg	Val	Ile	Gly	Gln	Arg	Lys	Ile	Leu	Pro	Asp	Pro
1				5					10				15		
Lys	Phe	Gly	Ser	Glu	Leu	Leu	Ala	Lys	Phe	Val	Asn	Ile	Leu	Met	Val
				20					25			30			
Asp	Gly	Lys	Lys	Ser	Thr	Ala	Glu	Ser	Ile	Val	Tyr	Ser	Ala	Leu	Glu
				35				40			45				
Thr	Leu	Ala	Gln	Arg	Ser	Gly	Lys	Ser	Glu	Leu	Glu	Ala	Phe	Glu	Val
				50				55			60				
Ala	Leu	Glu	Asn	Val	Arg	Pro	Thr	Val	Glu	Val	Lys	Ser	Arg	Arg	Val
				65				70			75			80	
Gly	Gly	Ser	Thr	Tyr	Gln	Val	Pro	Val	Glu	Val	Arg	Pro	Val	Arg	Arg
				85				90			95				
Asn	Ala	Leu	Ala	Met	Arg	Trp	Ile	Val	Glu	Ala	Ala	Arg	Lys	Arg	Gly
				100				105			110				
Asp	Lys	Ser	Met	Ala	Leu	Arg	Leu	Ala	Asn	Glu	Leu	Ser	Asp	Ala	Ala
				115				120			125				
Glu	Asn	Lys	Gly	Thr	Ala	Val	Lys	Lys	Arg	Glu	Asp	Val	His	Arg	Met
				130				135			140				
Ala	Glu	Ala	Asn	Lys	Ala	Phe	Ala	His	Tyr	Arg	Trp	Leu	Ser	Leu	Arg
				145				150			155			160	
Ser	Phe	Ser	His	Gln	Ala	Gly	Ala	Ser	Ser	Lys	Gln	Pro	Ala	Leu	Gly
				165				170			175				
Tyr	Leu	Asn													

<210> 250

<211> 124
<212> PRT
<213> E. Coli

<400> 250

Met Ala Thr Val Asn Gln Leu Val Arg Lys Pro Arg Ala Arg Lys Val
1 5 10 15
Ala Lys Ser Asn Val Pro Ala Leu Glu Ala Cys Pro Gln Lys Arg Gly
20 25 30
Val Cys Thr Arg Val Tyr Thr Thr Pro Lys Lys Pro Asn Ser Ala
35 40 45
Leu Arg Lys Val Cys Arg Val Arg Leu Thr Asn Gly Phe Glu Val Thr
50 55 60
Ser Tyr Ile Gly Gly Glu His Asn Leu Gln Glu His Ser Val Ile
65 70 75 80
Leu Ile Arg Gly Gly Arg Val Lys Asp Leu Pro Gly Val Arg Tyr His
85 90 95
Thr Val Arg Gly Ala Leu Asp Cys Ser Gly Val Lys Asp Arg Lys Gln
100 105 110
Ala Arg Ser Lys Tyr Gly Val Lys Arg Pro Lys Ala
115 120

<210> 251
<211> 165
<212> PRT
<213> E. Coli

<400> 251

Met Ala Leu Asn Leu Gln Asp Lys Gln Ala Ile Val Ala Glu Val Ser
1 5 10 15
Glu Val Ala Lys Gly Ala Leu Ser Ala Val Val Ala Asp Ser Arg Gly
20 25 30
Val Thr Val Asp Lys Met Thr Glu Leu Arg Lys Ala Gly Arg Glu Ala
35 40 45
Gly Val Tyr Met Arg Val Val Arg Asn Thr Leu Leu Arg Arg Ala Val
50 55 60
Glu Gly Thr Pro Phe Glu Cys Leu Lys Asp Ala Phe Val Gly Pro Thr
65 70 75 80
Leu Ile Ala Tyr Ser Met Glu His Pro Gly Ala Ala Ala Arg Leu Phe
85 90 95
Lys Glu Phe Ala Lys Ala Asn Ala Lys Phe Glu Val Lys Ala Ala Ala
100 105 110
Phe Glu Gly Glu Leu Ile Pro Ala Ser Gln Ile Asp Arg Leu Ala Thr
115 120 125
Leu Pro Thr Tyr Glu Glu Ala Ile Ala Arg Leu Met Ala Thr Met Lys
130 135 140
Glu Ala Ser Ala Gly Lys Leu Val Arg Thr Leu Ala Ala Val Arg Asp
145 150 155 160
Ala Lys Glu Ala Ala
165

<210> 252
<211> 121
<212> PRT
<213> E. Coli

<400> 252

Met Ser Ile Thr Lys Asp Gln Ile Ile Glu Ala Val Ala Ala Met Ser
1 5 10 15
Val Met Asp Val Val Glu Leu Ile Ser Ala Met Glu Glu Lys Phe Gly
20 25 30
Val Ser Ala Ala Ala Ala Val Ala Val Ala Ala Gly Pro Val Glu Ala
35 40 45
Ala Glu Glu Lys Thr Glu Phe Asp Val Ile Leu Lys Ala Ala Gly Ala
50 55 60
Asn Lys Val Ala Val Ile Lys Ala Val Arg Gly Ala Thr Gly Leu Gly
65 70 75 80
Leu Lys Glu Ala Lys Asp Leu Val Glu Ser Ala Pro Ala Ala Leu Lys
85 90 95
Glu Gly Val Ser Lys Asp Asp Ala Glu Ala Leu Lys Lys Ala Leu Glu
100 105 110
Glu Ala Gly Ala Glu Val Glu Val Lys
115 120

<210> 253

<211> 714

<212> PRT

<213> E. Coli

<400> 253

Met Ser Arg Ile Ile Met Leu Ile Pro Thr Gly Thr Ser Val Gly Leu
1 5 10 15
Thr Ser Val Ser Leu Gly Val Ile Arg Ala Met Glu Arg Lys Gly Val
20 25 30
Arg Leu Ser Val Phe Lys Pro Ile Ala Gln Pro Arg Thr Gly Gly Asp
35 40 45
Ala Pro Asp Gln Thr Thr Ile Val Arg Ala Asn Ser Ser Thr Thr
50 55 60
Thr Ala Ala Glu Pro Leu Lys Met Ser Tyr Val Glu Gly Leu Leu Ser
65 70 75 80
Ser Asn Gln Lys Asp Val Leu Met Glu Glu Ile Val Ala Asn Tyr His
85 90 95
Ala Asn Thr Lys Asp Ala Glu Val Val Leu Val Glu Gly Leu Val Pro
100 105 110
Thr Arg Lys His Gln Phe Ala Gln Ser Leu Asn Tyr Glu Ile Ala Lys
115 120 125
Thr Leu Asn Ala Glu Ile Val Phe Val Met Ser Gln Gly Thr Asp Thr
130 135 140
Pro Glu Gln Leu Lys Glu Arg Ile Glu Leu Thr Arg Asn Ser Phe Gly
145 150 155 160
Gly Ala Lys Asn Thr Asn Ile Thr Gly Val Ile Val Asn Lys Leu Asn
165 170 175
Ala Pro Val Asp Glu Gln Gly Arg Thr Arg Pro Asp Leu Ser Glu Ile
180 185 190
Phe Asp Asp Ser Ser Lys Ala Lys Val Asn Asn Val Asp Pro Ala Lys
195 200 205
Leu Gln Glu Ser Ser Pro Leu Pro Val Leu Gly Ala Val Pro Trp Ser
210 215 220
Phe Asp Leu Ile Ala Thr Arg Ala Ile Asp Met Ala Arg His Leu Asn
225 230 235 240
Ala Thr Ile Ile Asn Glu Gly Asp Ile Asn Thr Arg Arg Val Lys Ser

	245	250	255												
Val	Thr	Phe	Cys	Ala	Arg	Ser	Ile	Pro	His	Met	Leu	Glu	His	Phe	Arg
			260					265						270	
Ala	Gly	Ser	Leu	Leu	Val	Thr	Ser	Ala	Asp	Arg	Pro	Asp	Val	Leu	Val
			275				280						285		
Ala	Ala	Cys	Leu	Ala	Ala	Met	Asn	Gly	Val	Glu	Ile	Gly	Ala	Leu	Leu
			290			295				300					
Leu	Thr	Gly	Gly	Tyr	Glu	Met	Asp	Ala	Arg	Ile	Ser	Lys	Leu	Cys	Glu
			305		310				315				320		
Arg	Ala	Phe	Ala	Thr	Gly	Leu	Pro	Val	Phe	Met	Val	Asn	Thr	Asn	Thr
			325				330						335		
Trp	Gln	Thr	Ser	Leu	Ser.	Leu	Gln	Ser	Phe	Asn	Leu	Glu	Val	Pro	Val
			340				345						350		
Asp	Asp	His	Glu	Arg	Ile	Glu	Lys	Val	Gln	Glu	Tyr	Val	Ala	Asn	Tyr
			355			360					365				
Ile	Asn	Ala	Asp	Trp	Ile	Glu	Ser	Leu	Thr	Ala	Thr	Ser	Glu	Arg	Ser
			370			375				380					
Arg	Arg	Leu	Ser	Pro	Pro	Ala	Phe	Arg	Tyr	Gln	Leu	Thr	Glu	Leu	Ala
			385		390				395				400		
Arg	Lys	Ala	Gly	Lys	Arg	Ile	Val	Leu	Pro	Glu	Gly	Asp	Glu	Pro	Arg
			405				410						415		
Thr	Val	Lys	Ala	Ala	Ala	Ile	Cys	Ala	Glu	Arg	Gly	Ile	Ala	Thr	Cys
			420				425					430			
Val	Leu	Leu	Gly	Asn	Pro	Ala	Glu	Ile	Asn	Arg	Val	Ala	Ala	Ser	Gln
			435				440					445			
Gly	Val	Glu	Leu	Gly	Ala	Gly	Ile	Glu	Ile	Val	Asp	Pro	Glu	Val	Val
			450			455				460					
Arg	Glu	Ser	Tyr	Val	Gly	Arg	Leu	Val	Glu	Leu	Arg	Lys	Asn	Lys	Gly
			465		470				475				480		
Met	Thr	Glu	Thr	Val	Ala	Arg	Glu	Gln	Leu	Glu	Asp	Asn	Val	Val	Leu
			485				490						495		
Gly	Thr	Leu	Met	Leu	Glu	Gln	Asp	Glu	Val	Asp	Gly	Leu	Val	Ser	Gly
			500			505						510			
Ala	Val	His	Thr	Thr	Ala	Asn	Thr	Ile	Arg	Pro	Pro	Leu	Gln	Leu	Ile
			515			520						525			
Lys	Thr	Ala	Pro	Gly	Ser	Ser	Leu	Val	Ser	Ser	Val	Phe	Phe	Met	Leu
			530			535						540			
Leu	Pro	Glu	Gln	Val	Tyr	Val	Tyr	Gly	Asp	Cys	Ala	Ile	Asn	Pro	Asp
			545		550				555				560		
Pro	Thr	Ala	Glu	Gln	Leu	Ala	Glu	Ile	Ala	Ile	Gln	Ser	Ala	Asp	Ser
			565			570						575			
Ala	Ala	Ala	Phe	Gly	Ile	Glu	Pro	Arg	Val	Ala	Met	Leu	Ser	Tyr	Ser
			580			585						590			
Thr	Gly	Thr	Ser	Gly	Ala	Gly	Ser	Asp	Val	Glu	Lys	Val	Arg	Glu	Ala
			595			600						605			
Thr	Arg	Leu	Ala	Gln	Glu	Lys	Arg	Pro	Asp	Leu	Met	Ile	Asp	Gly	Pro
			610			615						620			
Leu	Gln	Tyr	Asp	Ala	Ala	Val	Met	Ala	Asp	Val	Ala	Lys	Ser	Lys	Ala
			625		630				635				640		
Pro	Asn	Ser	Pro	Val	Ala	Gly	Arg	Ala	Thr	Val	Phe	Ile	Phe	Pro	Asp
			645			650						655			
Leu	Asn	Thr	Gly	Asn	Thr	Thr	Tyr	Lys	Ala	Val	Gln	Arg	Ser	Ala	Asp
			660			665						670			
Leu	Ile	Ser	Ile	Gly	Pro	Met	Leu	Gln	Gly	Met	Arg	Lys	Pro	Val	Asn
			675			680						685			
Asp	Leu	Ser	Arg	Gly	Ala	Leu	Val	Asp	Asp	Ile	Val	Tyr	Thr	Ile	Ala
			690			695						700			

Leu Thr Ala Ile Gln Ser Ala Gln Gln Gln
705 710

<210> 254
<211> 588
<212> PRT
<213> E. Coli

<400> 254
Met Asn Asn Ser Ile Asn His Lys Phe His His Ile Ser Arg Ala Glu
1 5 10 15
Tyr Gln Glu Leu Leu Ala Val Ser Arg Gly Asp Ala Val Ala Asp Tyr
20 25 30
Ile Ile Asp Asn Val Ser Ile Leu Asp Leu Ile Asn Gly Gly Glu Ile
35 40 45
Ser Gly Pro Ile Val Ile Lys Gly Arg Tyr Ile Ala Gly Val Gly Ala
50 55 60
Glu Tyr Thr Asp Ala Pro Ala Leu Gln Arg Ile Asp Ala Arg Gly Ala
65 70 75 80
Thr Ala Val Pro Gly Phe Ile Asp Ala His Leu His Ile Glu Ser Ser
85 90 95
Met Met Thr Pro Val Thr Phe Glu Thr Ala Thr Leu Pro Arg Gly Leu
100 105 110
Thr Thr Val Ile Cys Asp Pro His Glu Ile Val Asn Val Met Gly Glu
115 120 125
Ala Gly Phe Ala Trp Phe Ala Arg Cys Ala Glu Gln Ala Arg Gln Asn
130 135 140
Gln Tyr Leu Gln Val Ser Ser Cys Val Pro Ala Leu Glu Gly Cys Asp
145 150 155 160
Val Asn Gly Ala Ser Phe Thr Leu Glu Gln Met Leu Ala Trp Arg Asp
165 170 175
His Pro Gln Val Thr Gly Leu Ala Glu Met Met Asp Tyr Pro Gly Val
180 185 190
Ile Ser Gly Gln Asn Ala Leu Leu Asp Lys Leu Asp Ala Phe Arg His
195 200 205
Leu Thr Leu Asp Gly His Cys Pro Gly Leu Gly Gly Lys Glu Leu Asn
210 215 220
Ala Tyr Ile Thr Ala Gly Ile Glu Asn Cys His Glu Ser Tyr Gln Leu
225 230 235 240
Glu Glu Gly Arg Arg Lys Leu Gln Leu Gly Met Ser Leu Met Ile Arg
245 250 255
Glu Gly Ser Ala Ala Arg Asn Leu Asn Ala Leu Ala Pro Leu Ile Asn
260 265 270
Glu Phe Asn Ser Pro Gln Cys Met Leu Cys Thr Asp Asp Arg Asn Pro
275 280 285
Trp Glu Ile Ala His Glu Gly His Ile Asp Ala Leu Ile Arg Arg Leu
290 295 300
Ile Glu Gln His Asn Val Pro Leu His Val Ala Tyr Arg Val Ala Ser
305 310 315 320
Trp Ser Thr Ala Arg His Phe Gly Leu Asn His Leu Gly Leu Leu Ala
325 330 335
Pro Gly Lys Gln Ala Asp Ile Val Leu Leu Ser Asp Ala Arg Lys Val
340 345 350
Thr Val Gln Gln Val Leu Val Lys Gly Glu Pro Ile Asp Ala Gln Thr
355 360 365
Leu Gln Ala Glu Glu Ser Ala Arg Leu Ala Gln Ser Ala Pro Pro Tyr

370	375	380
Gly Asn Thr Ile Ala Arg Gln Pro Val Ser Ala Ser Asp Phe Ala Leu		
385	390	395 400
Gln Phe Thr Pro Gly Lys Arg Tyr Arg Val Ile Asp Val Ile His Asn		
405	410	415
Glu Leu Ile Thr His Ser His Ser Ser Val Tyr Ser Glu Asn Gly Phe		
420	425	430
Asp Arg Asp Asp Val Ser Phe Ile Ala Val Leu Glu Arg Tyr Gly Gln		
435	440	445
Arg Leu Ala Pro Ala Cys Gly Leu Leu Gly Gly Phe Gly Leu Asn Glu		
450	455	460
Gly Ala Leu Ala Ala Thr Val Ser His Asp Ser His Asn Ile Val Val		
465	470	475 480
Ile Gly Arg Ser Ala Glu Glu Met Ala Leu Ala Val Asn Gln Val Ile		
485	490	495
Gln Asp Gly Gly Leu Cys Val Val Arg Asn Gly Gln Val Gln Ser		
500	505	510
His Leu Pro Leu Pro Ile Ala Gly Leu Met Ser Thr Asp Thr Ala Gln		
515	520	525
Ser Leu Ala Glu Gln Ile Asp Ala Leu Lys Ala Ala Ala Arg Glu Cys		
530	535	540
Gly Pro Leu Pro Asp Glu Pro Phe Ile Gln Met Ala Phe Leu Ser Leu		
545	550	555 560
Pro Val Ile Pro Ala Leu Lys Leu Thr Ser Gln Gly Leu Phe Asp Gly		
565	570	575
Glu Lys Phe Ala Phe Thr Thr Leu Glu Val Thr Glu		
580	585	

<210> 255
<211> 408
<212> PRT
<213> E. Coli

<400> 255

Met Ala Tyr Cys Asn Pro Gly Leu Glu Ser Arg Pro Asn Lys Arg Asn		
1	5	10 15
Ala Leu Arg Arg His Val Val Thr Gly Ile Gly Met Lys Ile Val Ile		
20	25	30
Ala Pro Asp Ser Tyr Lys Glu Ser Leu Ser Ala Ser Glu Val Ala Gln		
35	40	45
Ala Ile Glu Lys Gly Phe Arg Glu Ile Phe Pro Asp Ala Gln Tyr Val		
50	55	60
Ser Val Pro Val Ala Asp Gly Gly Glu Gly Thr Val Glu Ala Met Ile		
65	70	75 80
Ala Ala Thr Gln Gly Ala Glu Arg His Ala Trp Val Thr Gly Pro Leu		
85	90	95
Gly Glu Lys Val Asn Ala Ser Trp Gly Ile Ser Gly Asp Gly Lys Thr		
100	105	110
Ala Phe Ile Glu Met Ala Ala Ser Gly Leu Glu Leu Val Pro Ala		
115	120	125
Glu Lys Arg Asp Pro Leu Val Thr Thr Ser Arg Gly Thr Gly Glu Leu		
130	135	140
Ile Leu Gln Ala Leu Glu Ser Gly Ala Thr Asn Ile Ile Ile Gly Ile		
145	150	155 160
Gly Gly Ser Ala Thr Asn Asp Gly Gly Ala Gly Met Val Gln Ala Leu		
165	170	175

Gly Ala Lys Leu Cys Asp Ala Asn Gly Asn Glu Ile Gly Phe Gly Gly
 180 185 190
 Gly Ser Leu Asn Thr Leu Asn Asp Ile Asp Ile Ser Gly Leu Asp Pro
 195 200 205
 Arg Leu Lys Asp Cys Val Ile Arg Val Ala Cys Asp Val Thr Asn Pro
 210 215 220
 Leu Val Gly Asp Asn Gly Ala Ser Arg Ile Phe Gly Pro Gln Lys Gly
 225 230 235 240
 Ala Ser Glu Ala Met Ile Val Glu Leu Asp Asn Asn Leu Ser His Tyr
 245 250 255
 Ala Glu Val Ile Lys Lys Ala Leu His Val Asp Val Lys Asp Val Pro
 260 265 270
 Gly Ala Gly Ala Ala Gly Gly Met Gly Ala Ala Leu Met Ala Phe Leu
 275 280 285
 Gly Ala Glu Leu Lys Ser Gly Ile Glu Ile Val Thr Thr Ala Leu Asn
 290 295 300
 Leu Glu Glu His Ile His Asp Cys Thr Leu Val Ile Thr Gly Glu Gly
 305 310 315 320
 Arg Ile Asp Ser Gln Ser Ile His Gly Lys Val Pro Ile Gly Val Ala
 325 330 335
 Asn Val Ala Lys Lys Tyr His Lys Pro Val Ile Gly Ile Ala Gly Ser
 340 345 350
 Leu Thr Asp Asp Val Gly Val Val His Gln His Gly Ile Asp Ala Val
 355 360 365
 Phe Ser Val Leu Thr Ser Ile Gly Thr Leu Asp Glu Ala Phe Arg Gly
 370 375 380
 Ala Tyr Asp Asn Ile Cys Arg Ala Ser Arg Asn Ile Ala Ala Thr Leu
 385 390 395 400
 Ala Ile Gly Met Arg Asn Ala Gly
 405

<210> 256
 <211> 299
 <212> PRT
 <213> E. Coli

<400> 256

Met Ile Asp Met Thr Met Lys Val Gly Phe Ile Gly Leu Gly Ile Met
 1 5 10 15
 Gly Lys Pro Met Ser Lys Asn Leu Leu Lys Ala Gly Tyr Ser Leu Val
 20 25 30
 Val Ala Asp Arg Asn Pro Glu Ala Ile Ala Asp Val Ile Ala Ala Gly
 35 40 45
 Ala Glu Thr Ala Ser Thr Ala Lys Ala Ile Ala Glu Gln Cys Asp Val
 50 55 60
 Ile Ile Thr Met Leu Pro Asn Ser Pro His Val Lys Glu Val Ala Leu
 65 70 75 80
 Gly Glu Asn Gly Ile Ile Glu Gly Ala Lys Pro Gly Thr Val Leu Ile
 85 90 95
 Asp Met Ser Ser Ile Ala Pro Leu Ala Ser Arg Glu Ile Ser Glu Ala
 100 105 110
 Leu Lys Ala Lys Gly Ile Asp Met Leu Asp Ala Pro Val Ser Gly Gly
 115 120 125
 Glu Pro Lys Ala Ile Asp Gly Thr Leu Ser Val Met Val Gly Gly Asp
 130 135 140
 Lys Ala Ile Phe Asp Lys Tyr Tyr Asp Leu Met Lys Ala Met Ala Gly

145	150	155	160
Ser Val Val His Thr Gly Glu Ile Gly Ala Gly Asn Val Thr Lys Leu			
165	170	175	
Ala Asn Gln Val Ile Val Ala Leu Asn Ile Ala Ala Met Ser Glu Ala			
180	185	190	
Leu Thr Leu Ala Thr Lys Ala Gly Val Asn Pro Asp Leu Val Tyr Gln			
195	200	205	
Ala Ile Arg Gly Gly Leu Ala Gly Ser Thr Val Leu Asp Ala Lys Ala			
210	215	220	
Pro Met Val Met Asp Arg Asn Phe Lys Pro Gly Phe Arg Ile Asp Leu			
225	230	235	240
His Ile Lys Asp Leu Ala Asn Ala Leu Asp Thr Ser His Gly Val Gly			
245	250	255	
Ala Gln Leu Pro Leu Thr Ala Ala Val Met Glu Met Met Gln Ala Leu			
260	265	270	
Arg Ala Asp Gly Leu Gly Thr Ala Asp His Ser Ala Leu Ala Cys Tyr			
275	280	285	
Tyr Glu Lys Leu Ala Lys Val Glu Val Thr Arg			
290	295		

<210> 257
<211> 256
<212> PRT
<213> E. Coli

<400> 257			
Met Asn Asn Asp Val Phe Pro Asn Lys Phe Lys Ala Ala Leu Ala Ala			
1	5	10	15
Lys Gln Val Gln Ile Gly Cys Trp Ser Ala Leu Ser Asn Pro Ile Ser			
20	25	30	
Thr Glu Val Leu Gly Leu Ala Gly Phe Asp Trp Leu Val Leu Asp Gly			
35	40	45	
Glu His Ala Pro Asn Asp Ile Ser Thr Phe Ile Pro Gln Leu Met Ala			
50	55	60	
Leu Lys Gly Ser Ala Ser Ala Pro Val Val Arg Val Pro Thr Asn Glu			
65	70	75	80
Pro Val Ile Ile Lys Arg Leu Leu Asp Ile Gly Phe Tyr Asn Phe Leu			
85	90	95	
Ile Pro Phe Val Glu Thr Lys Glu Glu Ala Glu Leu Ala Val Ala Ser			
100	105	110	
Thr Arg Tyr Pro Pro Glu Gly Ile Arg Gly Val Ser Val Ser His Arg			
115	120	125	
Ala Asn Met Phe Gly Thr Val Ala Asp Tyr Phe Ala Gln Ser Asn Lys			
130	135	140	
Asn Ile Thr Ile Leu Val Gln Ile Glu Ser Gln Gln Gly Val Asp Asn			
145	150	155	160
Val Asp Ala Ile Ala Ala Thr Glu Gly Val Asp Gly Ile Phe Val Gly			
165	170	175	
Pro Ser Asp Leu Ala Ala Leu Gly His Leu Gly Asn Ala Ser His			
180	185	190	
Pro Asp Val Gln Lys Ala Ile Gln His Ile Phe Asn Arg Ala Ser Ala			
195	200	205	
His Gly Lys Pro Ser Gly Ile Leu Ala Pro Val Glu Ala Asp Ala Arg			
210	215	220	
Arg Tyr Leu Glu Trp Gly Ala Thr Phe Val Ala Val Gly Ser Asp Leu			

225	230	235	240
Gly Val Phe Arg Ser Ala Thr Gln Lys Leu Ala Asp Thr Phe Lys Lys			
245	250	255	

<210> 258

<211> 444

<212> PRT

<213> E. Coli

<400> 258

Met Ile Leu Asp Thr Val Asp Glu Lys Lys Gly Val His Thr Arg			
1	5	10	15
Tyr Leu Ile Leu Ile Ile Phe Ile Val Thr Ala Val Asn Tyr Ala			
20	25	30	
Asp Arg Ala Thr Leu Ser Ile Ala Gly Thr Glu Val Ala Lys Glu Leu			
35	40	45	
Gln Leu Ser Ala Val Ser Met Gly Tyr Ile Phe Ser Ala Phe Gly Trp			
50	55	60	
Ala Tyr Leu Leu Met Gln Ile Pro Gly Gly Trp Leu Leu Asp Lys Phe			
65	70	75	80
Gly Ser Lys Lys Val Tyr Thr Tyr Ser Leu Phe Phe Trp Ser Leu Phe			
85	90	95	
Thr Phe Leu Gln Gly Phe Val Asp Met Phe Pro Leu Ala Trp Ala Gly			
100	105	110	
Ile Ser Met Phe Phe Met Arg Phe Met Leu Gly Phe Ser Glu Ala Pro			
115	120	125	
Ser Phe Pro Ala Asn Ala Arg Ile Val Ala Ala Trp Phe Pro Thr Lys			
130	135	140	
Glu Arg Gly Thr Ala Ser Ala Ile Phe Asn Ser Ala Gln Tyr Phe Ser			
145	150	155	160
Leu Ala Leu Phe Ser Pro Leu Leu Gly Trp Leu Thr Phe Ala Trp Gly			
165	170	175	
Trp Glu His Val Phe Thr Val Met Gly Val Ile Gly Phe Val Leu Thr			
180	185	190	
Ala Leu Trp Ile Lys Leu Ile His Asn Pro Thr Asp His Pro Arg Met			
195	200	205	
Ser Ala Glu Glu Leu Lys Phe Ile Ser Glu Asn Gly Ala Val Val Asp			
210	215	220	
Met Asp His Lys Lys Pro Gly Ser Ala Ala Ser Gly Pro Lys Leu			
225	230	235	240
His Tyr Ile Lys Gln Leu Leu Ser Asn Arg Met Met Leu Gly Val Phe			
245	250	255	
Phe Gly Gln Tyr Phe Ile Asn Thr Ile Thr Trp Phe Phe Leu Thr Trp			
260	265	270	
Phe Pro Ile Tyr Leu Val Gln Glu Lys Gly Met Ser Ile Leu Lys Val			
275	280	285	
Gly Leu Val Ala Ser Ile Pro Ala Leu Cys Gly Phe Ala Gly Gly Val			
290	295	300	
Leu Gly Gly Val Phe Ser Asp Tyr Leu Ile Lys Arg Gly Leu Ser Leu			
305	310	315	320
Thr Leu Ala Arg Lys Leu Pro Ile Val Leu Gly Met Leu Leu Ala Ser			
325	330	335	
Thr Ile Ile Leu Cys Asn Tyr Thr Asn Asn Thr Thr Leu Val Val Met			
340	345	350	
Leu Met Ala Leu Ala Phe Phe Gly Lys Gly Phe Gly Ala Leu Gly Trp			
355	360	365	

Pro	Val	Ile	Ser	Asp	Thr	Ala	Pro	Lys	Glu	Ile	Val	Gly	Leu	Cys	Gly
370							375					380			
Gly	Val	Phe	Asn	Val	Phe	Gly	Asn	Val	Ala	Ser	Ile	Val	Thr	Pro	Leu
385						390				395					400
Val	Ile	Gly	Tyr	Leu	Val	Ser	Glu	Leu	His	Ser	Phe	Asn	Ala	Ala	Leu
						405				410					415
Val	Phe	Val	Gly	Cys	Ser	Ala	Leu	Met	Ala	Met	Val	Cys	Tyr	Leu	Phe
						420			425						430
Val	Val	Gly	Asp	Ile	Lys	Arg	Met	Glu	Leu	Gln	Lys				
						435			440						

<210> 259
<211> 511
<212> PRT
<213> E. Coli

<400> 259															
Met	Gln	Thr	Ser	Asp	Thr	Arg	Ala	Leu	Pro	Leu	Leu	Cys	Ala	Arg	Ser
1							5			10					15
Val	Tyr	Lys	Gln	Tyr	Ser	Gly	Val	Asn	Val	Leu	Lys	Gly	Ile	Asp	Phe
							20			25					30
Thr	Leu	His	Gln	Gly	Glu	Val	His	Ala	Leu	Leu	Gly	Gly	Asn	Gly	Ala
							35			40					45
Gly	Lys	Ser	Thr	Leu	Met	Lys	Ile	Ile	Ala	Gly	Ile	Thr	Pro	Ala	Asp
							50			55					60
Ser	Gly	Thr	Leu	Glu	Ile	Glu	Gly	Asn	Asn	Tyr	Val	Arg	Leu	Thr	Pro
							65			70					80
Val	His	Ala	His	Gln	Leu	Gly	Ile	Tyr	Leu	Val	Pro	Gln	Glu	Pro	Leu
							85			90					95
Leu	Phe	Pro	Ser	Leu	Ser	Ile	Lys	Glu	Asn	Ile	Leu	Phe	Gly	Leu	Ala
							100			105					110
Lys	Lys	Gln	Leu	Ser	Met	Gln	Lys	Met	Lys	Asn	Leu	Leu	Ala	Ala	Leu
							115			120					125
Gly	Cys	Gln	Phe	Asp	Leu	His	Ser	Leu	Ala	Gly	Ser	Leu	Asp	Val	Ala
							130			135					140
Asp	Arg	Gln	Met	Val	Glu	Ile	Leu	Arg	Gly	Leu	Met	Arg	Asp	Ser	Arg
							145			150					160
Ile	Leu	Ile	Leu	Asp	Glu	Pro	Thr	Ala	Ser	Leu	Thr	Pro	Ala	Glu	Thr
							165			170					175
Glu	Arg	Leu	Phe	Ser	Arg	Leu	Gln	Glu	Leu	Leu	Ala	Thr	Gly	Val	Gly
							180			185					190
Ile	Val	Phe	Ile	Ser	His	Lys	Leu	Pro	Glu	Ile	Arg	Gln	Ile	Ala	Asp
							195			200					205
Arg	Ile	Ser	Val	Met	Arg	Asp	Gly	Thr	Ile	Ala	Leu	Ser	Gly	Lys	Thr
							210			215					220
Ser	Glu	Leu	Ser	Thr	Asp	Asp	Ile	Ile	Gln	Ala	Ile	Thr	Pro	Ala	Val
							225			230					240
Arg	Glu	Lys	Ser	Leu	Ser	Ala	Ser	Gln	Lys	Leu	Trp	Leu	Glu	Leu	Pro
							245			250					255
Gly	Asn	Arg	Pro	Gln	His	Ala	Ala	Gly	Thr	Pro	Val	Leu	Thr	Leu	Glu
							260			265					270
Asn	Leu	Thr	Gly	Glu	Gly	Phe	Arg	Asn	Val	Ser	Leu	Thr	Leu	Asn	Ala
							275			280					285
Gly	Glu	Ile	Leu	Gly	Leu	Ala	Gly	Leu	Val	Gly	Ala	Gly	Arg	Thr	Glu
							290			295					300
Leu	Ala	Glu	Thr	Leu	Tyr	Gly	Leu	Arg	Thr	Leu	Arg	Gly	Gly	Arg	Ile

305	310	315	320
Met Leu Asn Gly Lys Glu Ile Asn Lys Leu Ser Thr Gly Glu Arg Leu			
325	330	335	
Leu Arg Gly Leu Val Tyr Leu Pro Glu Asp Arg Gln Ser Ser Gly Leu			
340	345	350	
Asn Leu Asp Ala Ser Leu Ala Trp Asn Val Cys Ala Leu Thr His Asn			
355	360	365	
Leu Arg Gly Phe Trp Ala Lys Thr Ala Lys Asp Asn Ala Thr Leu Glu			
370	375	380	
Arg Tyr Arg Arg Ala Leu Asn Ile Lys Phe Asn Gln Pro Glu Gln Ala			
385	390	395	400
Ala Arg Thr Leu Ser Gly Gly Asn Gln Gln Lys Ile Leu Ile Ala Lys			
405	410	415	
Cys Leu Glu Ala Ser Pro Gln Val Leu Ile Val Asp Glu Pro Thr Arg			
420	425	430	
Gly Val Asp Val Ser Ala Arg Asn Asp Ile Tyr Gln Leu Leu Arg Ser			
435	440	445	
Ile Ala Ala Gln Asn Val Ala Val Leu Leu Ile Ser Ser Asp Leu Glu			
450	455	460	
Glu Ile Glu Leu Met Ala Asp Arg Val Tyr Val Met His Gln Gly Glu			
465	470	475	480
Ile Thr His Ser Ala Leu Thr Glu Arg Asp Ile Asn Val Glu Thr Ile			
485	490	495	
Met Arg Val Ala Phe Gly Asp Ser Gln Arg Gln Glu Ala Ser Cys			
500	505	510	

<210> 260
<211> 342
<212> PRT
<213> E. Coli

<400> 260			
Met Leu Lys Phe Ile Gln Asn Asn Arg Glu Ile Thr Ala Leu Leu Ala			
1	5	10	15
Val Val Leu Leu Phe Val Leu Pro Gly Phe Leu Asp Arg Gln Tyr Leu			
20	25	30	
Ser Val Gln Thr Leu Thr Met Val Tyr Ser Ser Ala Gln Ile Leu Ile			
35	40	45	
Leu Leu Ala Met Gly Ala Thr Leu Val Met Leu Thr Arg Asn Ile Asp			
50	55	60	
Val Ser Val Gly Ser Ile Thr Gly Met Cys Ala Val Leu Leu Gly Met			
65	70	75	80
Leu Leu Asn Ala Gly Tyr Ser Leu Pro Val Ala Cys Val Ala Thr Leu			
85	90	95	
Leu Leu Gly Leu Leu Ala Gly Phe Phe Asn Gly Val Leu Val Ala Trp			
100	105	110	
Leu Lys Ile Pro Ala Ile Val Ala Thr Leu Gly Thr Leu Gly Leu Tyr			
115	120	125	
Arg Gly Ile Met Leu Leu Trp Thr Gly Gly Lys Trp Ile Glu Gly Leu			
130	135	140	
Pro Ala Glu Leu Lys Gln Leu Ser Ala Pro Leu Leu Gly Val Ser			
145	150	155	160
Ala Ile Gly Trp Leu Thr Ile Ile Leu Val Ala Phe Met Ala Trp Leu			
165	170	175	
Leu Ala Lys Thr Ala Phe Gly Arg Ser Phe Tyr Ala Thr Gly Asp Asn			
180	185	190	

Leu Gln Gly Ala Arg Gln Leu Gly Val Arg Thr Glu Ala Ile Arg Ile
 195 200 205
 Val Ala Phe Ser Leu Asn Gly Cys Met Ala Ala Leu Ala Gly Ile Val
 210 215 220
 Phe Ala Ser Gln Ile Gly Phe Ile Pro Asn Gln Thr Gly Thr Gly Leu
 225 230 235 240
 Glu Met Lys Ala Ile Ala Ala Cys Val Leu Gly Gly Ile Ser Leu Leu
 245 250 255
 Gly Gly Ser Gly Ala Ile Ile Gly Ala Val Leu Gly Ala Trp Phe Leu
 260 265 270
 Thr Gln Ile Asp Ser Val Leu Val Leu Arg Ile Pro Ala Trp Trp
 275 280 285
 Asn Asp Phe Ile Ala Gly Leu Val Leu Leu Ala Val Leu Val Phe Asp
 290 295 300
 Gly Arg Leu Arg Cys Ala Leu Glu Arg Asn Leu Arg Arg Gln Lys Tyr
 305 310 315 320
 Ala Arg Phe Met Thr Pro Pro Pro Ser Val Lys Pro Ala Ser Ser Gly
 325 330 335
 Lys Lys Arg Glu Ala Ala
 340

<210> 261
 <211> 330
 <212> PRT
 <213> E. Coli

<400> 261

Met Arg Ile Arg Tyr Gly Trp Glu Leu Ala Leu Ala Leu Leu Val
 1 5 10 15
 Ile Glu Ile Val Ala Phe Gly Ala Ile Asn Pro Arg Met Leu Asp Leu
 20 25 30
 Asn Met Leu Leu Phe Ser Thr Ser Asp Phe Ile Cys Ile Gly Ile Val
 35 40 45
 Ala Leu Pro Leu Thr Met Val Ile Val Ser Gly Gly Ile Asp Ile Ser
 50 55 60
 Phe Gly Ser Thr Ile Gly Leu Cys Ala Ile Ala Leu Gly Val Leu Phe
 65 70 75 80
 Gln Ser Gly Val Pro Met Pro Leu Ala Ile Leu Leu Thr Leu Leu
 85 90 95
 Gly Ala Leu Cys Gly Leu Ile Asn Ala Gly Leu Ile Ile Tyr Thr Lys
 100 105 110
 Val Asn Pro Leu Val Ile Thr Leu Gly Thr Leu Tyr Leu Phe Ala Gly
 115 120 125
 Ser Ala Leu Leu Leu Ser Gly Met Ala Gly Ala Thr Gly Tyr Glu Gly
 130 135 140
 Ile Gly Gly Phe Pro Met Ala Phe Thr Asp Phe Ala Asn Leu Asp Val
 145 150 155 160
 Leu Gly Leu Pro Val Pro Leu Ile Ile Phe Leu Ile Cys Leu Leu Val
 165 170 175
 Phe Trp Leu Trp Leu His Lys Thr His Ala Gly Arg Asn Val Phe Leu
 180 185 190
 Ile Gly Gln Ser Pro Arg Val Ala Leu Tyr Ser Ala Ile Pro Val Asn
 195 200 205
 Arg Thr Leu Cys Ala Leu Tyr Ala Met Thr Gly Leu Ala Ser Ala Val
 210 215 220
 Ala Ala Val Leu Leu Val Ser Tyr Phe Gly Ser Ala Arg Ser Asp Leu
 225 230 235 240

Gly	Ala	Ser	Phe	Leu	Met	Pro	Ala	Ile	Thr	Ala	Val	Val	Leu	Gly	Gly
					245					250					255
Ala	Asn	Ile	Tyr	Gly	Gly	Ser	Gly	Ser	Ile	Ile	Gly	Thr	Ala	Ile	Ala
					260				265						270
Val	Leu	Leu	Val	Gly	Tyr	Leu	Gln	Gln	Gly	Leu	Gln	Met	Ala	Gly	Val
					275				280						285
Pro	Asn	Gln	Val	Ser	Ser	Ala	Leu	Ser	Gly	Ala	Leu	Leu	Ile	Val	Val
					290			295				300			
Val	Val	Gly	Arg	Ser	Val	Ser	Leu	His	Arg	Gln	Gln	Ile	Lys	Glu	Trp
					305		310			315					320
Leu	Ala	Arg	Arg	Ala	Asn	Asn	Pro	Leu	Pro						
					325				330						

<210> 262
 <211> 340
 <212> PRT
 <213> E. Coli

<400> 262																
Met	Thr	Leu	His	Arg	Phe	Lys	Lys	Ile	Ala	Leu	Leu	Ser	Ala	Leu	Gly	
1					5				10						15	
Ile	Ala	Ala	Ile	Ser	Met	Asn	Val	Gln	Ala	Ala	Glu	Arg	Ile	Ala	Phe	
								20			25				30	
Ile	Pro	Lys	Leu	Val	Gly	Val	Gly	Phe	Phe	Thr	Ser	Gly	Gly	Asn	Gly	
					35			40			45					
Ala	Gln	Gln	Ala	Gly	Lys	Glu	Leu	Gly	Val	Asp	Val	Thr	Tyr	Asp	Gly	
					50			55			60					
Pro	Thr	Glu	Pro	Ser	Val	Ser	Gly	Gln	Val	Gln	Leu	Ile	Asn	Asn	Phe	
					65			70			75				80	
Val	Asn	Gln	Gly	Tyr	Asn	Ala	Ile	Ile	Val	Ser	Ala	Val	Ser	Pro	Asp	
							85			90					95	
Gly	Leu	Cys	Pro	Ala	Leu	Lys	Arg	Ala	Met	Gln	Arg	Gly	Val	Arg	Val	
					100			105							110	
Leu	Thr	Trp	Asp	Ser	Asp	Thr	Lys	Pro	Glu	Cys	Arg	Ser	Tyr	Tyr	Ile	
					115			120							125	
Asn	Gln	Gly	Thr	Pro	Ala	Gln	Leu	Gly	Gly	Met	Leu	Val	Asp	Met	Ala	
					130			135			140					
Ala	Arg	Gln	Val	Asn	Lys	Asp	Lys	Ala	Lys	Val	Ala	Phe	Phe	Tyr	Ser	
					145			150			155				160	
Ser	Pro	Thr	Val	Thr	Asp	Gln	Asn	Gln	Trp	Val	Lys	Glu	Ala	Lys	Ala	
							165			170					175	
Lys	Ile	Ala	Lys	Glu	His	Pro	Gly	Trp	Glu	Ile	Val	Thr	Thr	Gln	Phe	
					180			185							190	
Gly	Tyr	Asn	Asp	Ala	Thr	Lys	Ser	Leu	Gln	Thr	Ala	Glu	Gly	Ile	Leu	
					195			200			205					
Lys	Ala	Tyr	Ser	Asp	Leu	Asp	Ala	Ile	Ile	Ala	Pro	Asp	Ala	Asn	Ala	
					210			215			220					
Leu	Pro	Ala	Ala	Ala	Gln	Ala	Ala	Glu	Asn	Leu	Lys	Asn	Asp	Lys	Val	
					225			230			235				240	
Ala	Ile	Val	Gly	Phe	Ser	Thr	Pro	Asn	Val	Met	Arg	Pro	Tyr	Val	Glu	
					245			250							255	
Arg	Gly	Thr	Val	Lys	Glu	Phe	Gly	Leu	Trp	Asp	Val	Val	Gln	Gln	Gly	
					260			265			270					
Lys	Ile	Ser	Val	Tyr	Val	Ala	Asp	Ala	Leu	Leu	Lys	Lys	Gly	Ser	Met	

275	280	285
Lys Thr Gly Asp Lys Leu Asp Ile Lys Gly Val Gly Gln Val Glu Val		
290	295	300
Ser Pro Asn Ser Val Gln Gly Tyr Asp Tyr Glu Ala Asp Gly Asn Gly		
305	310	315
Ile Val Leu Leu Pro Glu Arg Val Ile Phe Asn Lys Glu Asn Ile Gly		
325	330	335
Lys Tyr Asp Phe		
340		

<210> 263
<211> 291
<212> PRT
<213> E. Coli

<400> 263

Met Ala Asp Leu Asp Asp Ile Lys Asp Gly Lys Asp Phe Arg Thr Asp			
1	5	10	15
Gln Pro Gln Lys Asn Ile Pro Phe Thr Leu Lys Gly Cys Gly Ala Leu			
20	25	30	
Asp Trp Gly Met Gln Ser Arg Leu Ser Arg Ile Phe Asn Pro Lys Thr			
35	40	45	
Gly Lys Thr Val Met Leu Ala Phe Asp His Gly Tyr Phe Gln Gly Pro			
50	55	60	
Thr Thr Gly Leu Glu Arg Ile Asp Ile Asn Ile Ala Pro Leu Phe Glu			
65	70	75	80
His Ala Asp Val Leu Met Cys Thr Arg Gly Ile Leu Arg Ser Val Val			
85	90	95	
Pro Pro Ala Thr Asn Arg Pro Val Val Leu Arg Ala Ser Gly Ala Asn			
100	105	110	
Ser Ile Leu Ala Glu Leu Ser Asn Glu Ala Val Ala Leu Ser Met Asp			
115	120	125	
Asp Ala Val Arg Leu Asn Ser Cys Ala Val Ala Ala Gln Val Tyr Ile			
130	135	140	
Gly Ser Glu Tyr Glu His Gln Ser Ile Lys Asn Ile Ile Gln Leu Val			
145	150	155	160
Asp Ala Gly Met Lys Val Gly Met Pro Thr Met Ala Val Thr Gly Val			
165	170	175	
Gly Lys Asp Met Val Arg Asp Gln Arg Tyr Phe Ser Leu Ala Thr Arg			
180	185	190	
Ile Ala Ala Glu Met Gly Ala Gln Ile Ile Lys Thr Tyr Tyr Val Glu			
195	200	205	
Lys Gly Phe Glu Arg Ile Val Ala Gly Cys Pro Val Pro Ile Val Ile			
210	215	220	
Ala Gly Gly Lys Lys Leu Pro Glu Arg Glu Ala Leu Glu Met Cys Trp			
225	230	235	240
Gln Ala Ile Asp Gln Gly Ala Ser Gly Val Asp Met Gly Arg Asn Ile			
245	250	255	
Phe Gln Ser Asp His Pro Val Ala Met Met Lys Ala Val Gln Ala Val			
260	265	270	
Val His His Asn Glu Thr Ala Asp Arg Ala Tyr Glu Leu Tyr Leu Ser			
275	280	285	
Glu Lys Gln			
290			

<210> 264
<211> 96
<212> PRT
<213> E. Coli

<400> 264

Met His Val Thr Leu Val Glu Ile Asn Val His Glu Asp Lys Val Asp
1 5 10 15
Glu Phe Ile Glu Val Phe Arg Gln Asn His Leu Gly Ser Val Gln Glu
20 25 30
Glu Gly Asn Leu Arg Phe Asp Val Leu Gln Asp Pro Glu Val Asn Ser
35 40 45
Arg Phe Tyr Ile Tyr Glu Ala Tyr Lys Asp Glu Asp Ala Val Ala Phe
50 55 60
His Lys Thr Thr Pro His Tyr Lys Thr Cys Val Ala Lys Leu Glu Ser
65 70 75 80
Leu Met Thr Gly Pro Arg Lys Lys Arg Leu Phe Asn Gly Leu Met Pro
85 90 95

<210> 265

<211> 383

<212> PRT

<213> E. Coli

<400> 265

Met Phe Glu Pro Met Glu Leu Thr Asn Asp Ala Val Ile Lys Val Ile
1 5 10 15
Gly Val Gly Gly Gly Gly Asn Ala Val Glu His Met Val Arg Glu
20 25 30
Arg Ile Glu Gly Val Glu Phe Phe Ala Val Asn Thr Asp Ala Gln Ala
35 40 45
Leu Arg Lys Thr Ala Val Gly Gln Thr Ile Gln Ile Gly Ser Gly Ile
50 55 60
Thr Lys Gly Leu Gly Ala Gly Ala Asn Pro Glu Val Gly Arg Asn Ala
65 70 75 80
Ala Asp Glu Asp Arg Asp Ala Leu Arg Ala Ala Leu Glu Gly Ala Asp
85 90 95
Met Val Phe Ile Ala Ala Gly Met Gly Gly Thr Gly Thr Gly Ala
100 105 110
Ala Pro Val Val Ala Glu Val Ala Lys Asp Leu Gly Ile Leu Thr Val
115 120 125
Ala Val Val Thr Lys Pro Phe Asn Phe Glu Gly Lys Lys Arg Met Ala
130 135 140
Phe Ala Glu Gln Gly Ile Thr Glu Leu Ser Lys His Val Asp Ser Leu
145 150 155 160
Ile Thr Ile Pro Asn Asp Lys Leu Leu Lys Val Leu Gly Arg Gly Ile
165 170 175
Ser Leu Leu Asp Ala Phe Gly Ala Ala Asn Asp Val Leu Lys Gly Ala
180 185 190
Val Gln Gly Ile Ala Glu Leu Ile Thr Arg Pro Gly Leu Met Asn Val
195 200 205
Asp Phe Ala Asp Val Arg Thr Val Met Ser Glu Met Gly Tyr Ala Met
210 215 220
Met Gly Ser Gly Val Ala Ser Gly Glu Asp Arg Ala Glu Glu Ala Ala
225 230 235 240
Glu Met Ala Ile Ser Ser Pro Leu Leu Glu Asp Ile Asp Leu Ser Gly

	245	250	255
Ala Arg Gly Val Leu Val Asn Ile Thr Ala Gly Phe Asp Leu Arg Leu			
260	265	270	
Asp Glu Phe Glu Thr Val Gly Asn Thr Ile Arg Ala Phe Ala Ser Asp			
275	280	285	
Asn Ala Thr Val Val Ile Gly Thr Ser Leu Asp Pro Asp Met Asn Asp			
290	295	300	,
Glu Leu Arg Val Thr Val Val Ala Thr Gly Ile Gly Met Asp Lys Arg			
305	310	315	320
Pro Glu Ile Thr Leu Val Thr Asn Lys Gln Val Gln Gln Pro Val Met			
325	330	335	
Asp Arg Tyr Gln Gln His Gly Met Ala Pro Leu Thr Gln Glu Gln Lys			
340	345	350	
Pro Val Ala Lys Val Val Asn Asp Asn Ala Pro Gln Thr Ala Lys Glu			
355	360	365	
Pro Asp Tyr Leu Asp Ile Pro Ala Phe Leu Arg Lys Gln Ala Asp			
370	375	380	

<210> 266
 <211> 1014
 <212> PRT
 <213> E. Coli

	<400> 266		
Met Asp Val Ser Arg Arg Gln Phe Phe Lys Ile Cys Ala Gly Gly Met			
1	5	10	15
Ala Gly Thr Thr Val Ala Ala Leu Gly Phe Ala Pro Lys Gln Ala Leu			
20	25	30	
Ala Gln Ala Arg Asn Tyr Lys Leu Leu Arg Ala Lys Glu Ile Arg Asn			
35	40	45	
Thr Cys Thr Tyr Cys Ser Val Gly Cys Gly Leu Leu Met Tyr Ser Leu			
50	55	60	
Gly Asp Gly Ala Lys Asn Ala Arg Glu Ala Ile Tyr His Ile Glu Gly			
65	70	75	80
Asp Pro Asp His Pro Val Ser Arg Gly Ala Leu Cys Pro Lys Gly Ala			
85	90	95	
Gly Leu Leu Asp Tyr Val Asn Ser Glu Asn Arg Leu Arg Tyr Pro Glu			
100	105	110	
Tyr Arg Ala Pro Gly Ser Asp Lys Trp Gln Arg Ile Ser Trp Glu Glu			
115	120	125	
Ala Phe Ser Arg Ile Ala Lys Leu Met Lys Ala Asp Arg Asp Ala Asn			
130	135	140	
Phe Ile Glu Lys Asn Glu Gln Gly Val Thr Val Asn Arg Trp Leu Ser			
145	150	155	160
Thr Gly Met Leu Cys Ala Ser Gly Ala Ser Asn Glu Thr Gly Met Leu			
165	170	175	
Thr Gln Lys Phe Ala Arg Ser Leu Gly Met Leu Ala Val Asp Asn Gln			
180	185	190	
Ala Arg Val His Gly Pro Thr Val Ala Ser Leu Ala Pro Thr Phe Gly			
195	200	205	
Arg Gly Ala Met Thr Asn His Trp Val Asp Ile Lys Asn Ala Asn Val			
210	215	220	
Val Met Val Met Gly Gly Asn Ala Ala Glu Ala His Pro Val Gly Phe			
225	230	235	240
Arg Trp Ala Met Glu Ala Lys Asn Asn Asp Ala Thr Leu Ile Val			
245	250	255	

Val Asp Pro Arg Phe Thr Arg Thr Ala Ser Val Ala Asp Ile Tyr Ala
 260 265 270
 Pro Ile Arg Ser Gly Thr Asp Ile Thr Phe Leu Ser Gly Val Leu Arg
 275 280 285
 Tyr Leu Ile Glu Asn Asn Lys Ile Asn Ala Glu Tyr Val Lys His Tyr
 290 295 300
 Thr Asn Ala Ser Leu Leu Val Arg Asp Asp Phe Ala Phe Glu Asp Gly
 305 310 315 320
 Leu Phe Ser Gly Tyr Asp Ala Glu Lys Arg Gln Tyr Asp Lys Ser Ser
 325 330 335
 Trp Asn Tyr Gln Leu Asp Glu Asn Gly Tyr Ala Lys Arg Asp Glu Thr
 340 345 350
 Leu Thr His Pro Arg Cys Val Trp Asn Leu Leu Lys Glu His Val Ser
 355 360 365
 Arg Tyr Thr Pro Asp Val Val Glu Asn Ile Cys Gly Thr Pro Lys Ala
 370 375 380
 Asp Phe Leu Lys Val Cys Glu Val Leu Ala Ser Thr Ser Ala Pro Asp
 385 390 395 400
 Arg Thr Thr Thr Phe Leu Tyr Ala Leu Gly Trp Thr Gln His Thr Val
 405 410 415
 Gly Ala Gln Asn Ile Arg Thr Met Ala Met Ile Gln Leu Leu Gly
 420 425 430
 Asn Met Gly Met Ala Gly Gly Val Asn Ala Leu Arg Gly His Ser
 435 440 445
 Asn Ile Gln Gly Leu Thr Asp Leu Gly Leu Leu Ser Thr Ser Leu Pro
 450 455 460
 Gly Tyr Leu Thr Leu Pro Ser Glu Lys Gln Val Asp Leu Gln Ser Tyr
 465 470 475 480
 Leu Glu Ala Asn Thr Pro Lys Ala Thr Leu Ala Asp Gln Val Asn Tyr
 485 490 495
 Trp Ser Asn Tyr Pro Lys Phe Phe Val Ser Leu Met Lys Ser Phe Tyr
 500 505 510
 Gly Asp Ala Ala Gln Lys Glu Asn Asn Trp Gly Tyr Asp Trp Leu Pro
 515 520 525
 Lys Trp Asp Gln Thr Tyr Asp Val Ile Lys Tyr Phe Asn Met Met Asp
 530 535 540
 Glu Gly Lys Val Thr Gly Tyr Phe Cys Gln Gly Phe Asn Pro Val Ala
 545 550 555 560
 Ser Phe Pro Asp Lys Asn Lys Val Val Ser Cys Leu Ser Lys Leu Lys
 565 570 575
 Tyr Met Val Val Ile Asp Pro Leu Val Thr Glu Thr Ser Thr Phe Trp
 580 585 590
 Gln Asn His Gly Glu Ser Asn Asp Val Asp Pro Ala Ser Ile Gln Thr
 595 600 605
 Glu Val Phe Arg Leu Pro Ser Thr Cys Phe Ala Glu Glu Asp Gly Ser
 610 615 620
 Ile Ala Asn Ser Gly Arg Trp Leu Gln Trp His Trp Lys Gly Gln Asp
 625 630 635 640
 Ala Pro Gly Glu Ala Arg Asn Asp Gly Glu Ile Leu Ala Gly Ile Tyr
 645 650 655
 His His Leu Arg Glu Leu Tyr Gln Ser Glu Gly Gly Lys Gly Val Glu
 660 665 670
 Pro Leu Met Lys Met Ser Trp Asn Tyr Lys Gln Pro His Glu Pro Gln
 675 680 685
 Ser Asp Glu Val Ala Lys Glu Asn Asn Gly Tyr Ala Leu Glu Asp Leu
 690 695 700
 Tyr Asp Ala Asn Gly Val Leu Ile Ala Lys Lys Gln Leu Leu Ser

705	710	715	720
Ser Phe Ala His Leu Arg Asp Asp Gly Thr	Thr Ala Ser Ser Cys Trp		
725	730	735	
Ile Tyr Thr Gly Ser Trp Thr Glu Gln Gly Asn Gln Met Ala Asn Arg			
740	745	750	
Asp Asn Ser Asp Pro Ser Gly Leu Gly Asn Thr Leu Gly Trp Ala Trp			
755	760	765	
Ala Trp Pro Leu Asn Arg Arg Val Leu Tyr Asn Arg Ala Ser Ala Asp			
770	775	780	
Ile Asn Gly Lys Pro Trp Asp Pro Lys Arg Met Leu Ile Gln Trp Asn			
785	790	795	800
Gly Ser Lys Trp Thr Gly Asn Asp Ile Pro Asp Phe Gly Asn Ala Ala			
805	810	815	
Pro Gly Thr Pro Thr Gly Pro Phe Ile Met Gln Pro Glu Gly Met Gly			
820	825	830	
Arg Leu Phe Ala Ile Asn Lys Met Ala Glu Gly Pro Phe Pro Glu His			
835	840	845	
Tyr Glu Pro Ile Glu Thr Pro Leu Gly Thr Asn Pro Leu His Pro Asn			
850	855	860	
Val Val Ser Asn Pro Val Val Arg Leu Tyr Glu Gln Asp Ala Leu Arg			
865	870	875	880
Met Gly Lys Lys Glu Gln Phe Pro Tyr Val Gly Thr Thr Tyr Arg Leu			
885	890	895	
Thr Glu His Phe His Thr Trp Thr Lys His Ala Leu Leu Asn Ala Ile			
900	905	910	
Ala Gln Pro Glu Gln Phe Val Glu Ile Ser Glu Thr Leu Ala Ala Ala			
915	920	925	
Lys Gly Ile Asn Asn Gly Asp Arg Val Thr Val Ser Ser Lys Arg Gly			
930	935	940	
Phe Ile Arg Ala Val Ala Val Val Thr Arg Arg Leu Lys Pro Leu Asn			
945	950	955	960
Val Asn Gly Gln Gln Val Glu Thr Val Gly Ile Pro Ile His Trp Gly			
965	970	975	
Phe Glu Gly Val Ala Arg Lys Gly Tyr Ile Ala Asn Thr Leu Thr Pro			
980	985	990	
Asn Val Gly Asp Ala Asn Ser Gln Thr Pro Glu Tyr Lys Ala Phe Leu			
995	1000	1005	
Val Asn Ile Glu Lys Ala			
1010			

<210> 267
<211> 294
<212> PRT
<213> E. Coli

<400> 267

Met Ala Met Glu Thr Gln Asp Ile Ile Lys Arg Ser Ala Thr Asn Ser			
1	5	10	15
Ile Thr Pro Pro Ser Gln Val Arg Asp Tyr Lys Ala Glu Val Ala Lys			
20	25	30	
Leu Ile Asp Val Ser Thr Cys Ile Gly Cys Lys Ala Cys Gln Val Ala			
35	40	45	
Cys Ser Glu Trp Asn Asp Ile Arg Asp Glu Val Gly His Cys Val Gly			
50	55	60	
Val Tyr Asp Asn Pro Ala Asp Leu Ser Ala Lys Ser Trp Thr Val Met			
65	70	75	80
Arg Phe Ser Glu Thr Glu Gln Asn Gly Lys Leu Glu Trp Leu Ile Arg			

	85	90	95												
Lys	Asp	Gly	Cys	Met	His	Cys	Glu	Asp	Pro	Gly	Cys	Leu	Lys	Ala	Cys
				100				105					110		
Pro	Ser	Ala	Gly	Ala	Ile	Ile	Gln	Tyr	Ala	Asn	Gly	Ile	Val	Asp	Phe
				115				120					125		
Gln	Ser	Gl	Asn	Cys	Ile	Gly	Cys	Gly	Tyr	Cys	Ile	Ala	Gly	Cys	Pro
				130				135				140			
Phe	Asn	Ile	Pro	Arg	Leu	Asn	Glu	Asp	Asn	Arg	Val	Tyr	Lys	Cys	
				145				150			155		160		
Thr	Leu	Cys	Val	Asp	Arg	Val	Ser	Val	Gly	Gln	Glu	Pro	Ala	Cys	Val
				165				170				175			
Lys	Thr	Cys	Pro	Thr	Gly	Ala	Ile	His	Phe	Gly	Thr	Lys	Lys	Glu	Met
				180				185				190			
Leu	Glu	Leu	Ala	Glu	Gln	Arg	Val	Ala	Lys	Leu	Lys	Ala	Arg	Gly	Tyr
				195				200				205			
Glu	His	Ala	Gly	Val	Tyr	Asn	Pro	Glu	Gly	Val	Gly	Gly	Thr	His	Val
				210				215				220			
Met	Tyr	Val	Leu	His	His	Ala	Asp	Gln	Pro	Glu	Leu	Tyr	His	Gly	Leu
				225				230			235		240		
Pro	Lys	Asp	Pro	Lys	Ile	Asp	Thr	Ser	Val	Ser	Leu	Trp	Lys	Gly	Ala
				245				250				255			
Leu	Lys	Pro	Leu	Ala	Ala	Ala	Gly	Phe	Ile	Ala	Thr	Phe	Ala	Gly	Leu
				260				265				270			
Ile	Phe	His	Tyr	Ile	Gly	Ile	Gly	Pro	Asn	Lys	Glu	Val	Asp	Asp	Asp
				275				280				285			
Glu	Glu	Asp	His	His	Glu										
				290											

<210> 268
 <211> 217
 <212> PRT
 <213> E. Coli

	<400> 268														
Met	Ser	Lys	Ser	Lys	Met	Ile	Val	Arg	Thr	Lys	Phe	Ile	Asp	Arg	Ala
1					5				10				15		
Cys	His	Trp	Thr	Val	Val	Ile	Cys	Phe	Phe	Leu	Val	Ala	Leu	Ser	Gly
								20			25		30		
Ile	Ser	Phe	Phe	Phe	Pro	Thr	Leu	Gln	Trp	Leu	Thr	Gln	Thr	Phe	Gly
								35			40		45		
Thr	Pro	Gln	Met	Gly	Arg	Ile	Leu	His	Pro	Phe	Phe	Gly	Ile	Ala	Ile
								50			55		60		
Phe	Val	Ala	Leu	Met	Phe	Met	Phe	Val	Arg	Phe	Val	His	His	Asn	Ile
								65			70		75		80
Pro	Asp	Lys	Lys	Asp	Ile	Pro	Trp	Leu	Leu	Asn	Ile	Val	Glu	Val	Leu
								85			90		95		
Lys	Gly	Asn	Glu	His	Lys	Val	Ala	Asp	Val	Gly	Lys	Tyr	Asn	Ala	Gly
								100			105		110		
Gln	Lys	Met	Met	Phe	Trp	Ser	Ile	Met	Ser	Met	Ile	Phe	Val	Leu	Leu
								115			120		125		
Val	Thr	Gly	Val	Ile	Ile	Trp	Arg	Pro	Tyr	Phe	Ala	Gln	Tyr	Phe	Pro
								130			135		140		
Met	Gln	Val	Val	Arg	Tyr	Ser	Leu	Leu	Ile	His	Ala	Ala	Ala	Gly	Ile
								145			150		155		160
Ile	Leu	Ile	His	Ala	Ile	Leu	Ile	His	Met	Tyr	Met	Ala	Phe	Trp	Val
								165			170		175		

Lys	Gly	Ser	Ile	Lys	Gly	Met	Ile	Glu	Gly	Lys	Val	Ser	Arg	Arg	Trp
				180				185						190	
Ala	Lys	Lys	His	His	Pro	Arg	Trp	Tyr	Arg	Glu	Ile	Glu	Lys	Ala	Glu
				195				200					205		
Ala	Lys	Lys	Glu	Ser	Glu	Glu	Gly	Ile							
				210				215							

<210> 269

<211> 86

<212> PRT

<213> E. Coli

<400> 269

Met	Ala	Leu	Leu	Ile	Thr	Lys	Cys	Ile	Asn	Cys	Asp	Met	Cys	Glu	
1				5				10					15		
Pro	Glu	Cys	Pro	Asn	Glu	Ala	Ile	Ser	Met	Gly	Asp	His	Ile	Tyr	Glu
								20		25			30		
Ile	Asn	Ser	Asp	Lys	Cys	Thr	Glu	Cys	Val	Gly	His	Tyr	Glu	Thr	Pro
								35		40			45		
Thr	Cys	Gln	Lys	Val	Cys	Pro	Ile	Pro	Asn	Thr	Ile	Val	Lys	Asp	Pro
								50		55			60		
Ala	His	Val	Glu	Thr	Glu	Gln	Leu	Trp	Asp	Lys	Phe	Val	Leu	Met	
								65		70			75		80
His	His	Ala	Asp	Lys	Ile										
								85							

<210> 270

<211> 400

<212> PRT

<213> E. Coli

<400> 270

Met	Gln	Ser	Val	Asp	Val	Ala	Ile	Val	Gly	Gly	Met	Val	Gly	Leu	
1								5				10		15	
Ala	Val	Ala	Cys	Gly	Leu	Gln	Gly	Ser	Gly	Leu	Arg	Val	Ala	Val	Leu
								20		25			30		
Glu	Gln	Arg	Val	Gln	Glu	Pro	Leu	Ala	Ala	Asn	Ala	Pro	Pro	Gln	Leu
								35		40			45		
Arg	Val	Ser	Ala	Ile	Asn	Ala	Ala	Ser	Glu	Lys	Leu	Leu	Thr	Arg	Leu
								50		55			60		
Gly	Val	Trp	Gln	Asp	Ile	Leu	Ser	Arg	Arg	Ala	Ser	Cys	Tyr	His	Gly
								65		70			75		80
Met	Glu	Val	Trp	Asp	Lys	Asp	Ser	Phe	Gly	His	Ile	Ser	Phe	Asp	Asp
								85		90			95		
Gln	Ser	Met	Gly	Tyr	Ser	His	Leu	Gly	His	Ile	Val	Glu	Asn	Ser	Val
								100		105			110		
Ile	His	Tyr	Ala	Leu	Trp	Asn	Lys	Ala	His	Gln	Ser	Ser	Asp	Ile	Thr
								115		120			125		
Leu	Leu	Ala	Pro	Ala	Glu	Leu	Gln	Gln	Val	Ala	Trp	Gly	Glu	Asn	Glu
								130		135			140		
Thr	Phe	Leu	Thr	Leu	Lys	Asp	Gly	Ser	Met	Leu	Thr	Ala	Arg	Leu	Val
								145		150			155		160
Ile	Gly	Ala	Asp	Gly	Ala	Asn	Ser	Trp	Leu	Arg	Asn	Lys	Ala	Asp	Ile
								165		170			175		
Pro	Leu	Thr	Phe	Trp	Asp	Tyr	Gln	His	His	Ala	Leu	Val	Ala	Thr	Ile

180	185	190
Arg Thr Glu Glu Pro His Asp Ala Val Ala Arg Gln Val Phe His Gly		
195	200	205
Glu Gly Ile Leu Ala Phe Leu Pro Leu Ser Asp Pro His Leu Cys Ser		
210	215	220
Ile Val Trp Ser Leu Ser Pro Glu Glu Ala Gln Arg Met Gln Gln Ala		
225	230	235
Ser Glu Asp Glu Phe Asn Arg Ala Leu Asn Ile Ala Phe Asp Asn Arg		
245	250	255
Leu Gly Leu Cys Lys Val Glu Ser Ala Arg Gln Val Phe Pro Leu Thr		
260	265	270
Gly Arg Tyr Ala Arg Gln Phe Ala Ser His Arg Leu Ala Leu Val Gly		
275	280	285
Asp Ala Ala His Thr Ile His Pro Leu Ala Gly Gln Gly Val Asn Leu		
290	295	300
Gly Phe Met Asp Ala Ala Glu Leu Ile Ala Glu Leu Lys Arg Leu His		
305	310	315
Arg Gln Gly Lys Asp Ile Gly Gln Tyr Ile Tyr Leu Arg Arg Tyr Glu		
325	330	335
Arg Ser Arg Lys His Ser Ala Ala Leu Met Leu Ala Gly Met Gln Gly		
340	345	350
Phe Arg Asp Leu Phe Ser Gly Thr Asn Pro Ala Lys Lys Leu Leu Arg		
355	360	365
Asp Ile Gly Leu Lys Leu Ala Asp Thr Leu Pro Gly Val Lys Pro Gln		
370	375	380
Leu Ile Arg Gln Ala Met Gly Leu Asn Asp Leu Pro Glu Trp Leu Arg		
385	390	395
		400

<210> 271
 <211> 392
 <212> PRT
 <213> E. Coli

<400> 271		
Met Ser Val Ile Ile Val Gly Gly Gly Met Ala Gly Ala Thr Leu Ala		
1	5	10
Leu Ala Ile Ser Arg Leu Ser His Gly Ala Leu Pro Val His Leu Ile		
20	25	30
Glu Ala Thr Ala Pro Glu Ser His Ala His Pro Gly Phe Asp Gly Arg		
35	40	45
Ala Ile Ala Leu Ala Ala Gly Thr Cys Gln Gln Leu Ala Arg Ile Gly		
50	55	60
Val Trp Gln Ser Leu Ala Asp Cys Ala Thr Ala Ile Thr Thr Val His		
65	70	75
Val Ser Asp Arg Gly His Ala Gly Phe Val Thr Leu Ala Ala Glu Asp		
85	90	95
Tyr Gln Leu Ala Ala Leu Gly Gln Val Val Glu Leu His Asn Val Gly		
100	105	110
Gln Arg Leu Phe Ala Leu Leu Arg Lys Ala Pro Gly Val Thr Leu His		
115	120	125
Cys Pro Asp Arg Val Ala Asn Val Ala Arg Thr Gln Ser His Val Glu		
130	135	140
Val Thr Leu Glu Ser Gly Glu Thr Leu Thr Gly Arg Val Leu Val Ala		
145	150	155
Ala Asp Gly Thr His Ser Ala Leu Ala Thr Ala Cys Gly Val Asp Trp		
165	170	175

Gln Gln Glu Pro Tyr Glu Gln Leu Ala Val Ile Ala Asn Val Ala Thr
 180 185 190
 Ser Val Ala His Glu Gly Arg Ala Phe Glu Arg Phe Thr Gln His Gly
 195 200 205
 Pro Leu Ala Met Leu Pro Met Ser Asp Gly Arg Cys Ser Leu Val Trp
 210 215 220
 Cys His Pro Leu Glu Arg Arg Glu Glu Val Leu Ser Trp Ser Asp Glu
 225 230 235 240
 Lys Phe Cys Arg Glu Leu Gln Ser Ala Phe Gly Trp Arg Leu Gly Lys
 245 250 255
 Ile Thr His Ala Gly Lys Arg Ser Ala Tyr Pro Leu Ala Leu Thr His
 260 265 270
 Ala Ala Arg Ser Ile Thr His Arg Thr Val Leu Val Gly Asn Ala Ala
 275 280 285
 Gln Thr Leu His Pro Ile Ala Gly Gln Gly Phe Asn Leu Gly Met Arg
 290 295 300
 Asp Val Met Ser Leu Ala Glu Thr Leu Thr Gln Ala Gln Glu Arg Gly
 305 310 315 320
 Glu Asp Met Gly Asp Tyr Gly Val Leu Cys Arg Tyr Gln Gln Arg Arg
 325 330 335
 Gln Ser Asp Arg Glu Ala Thr Ile Gly Val Thr Asp Ser Leu Val His
 340 345 350
 Leu Phe Ala Asn Arg Trp Ala Pro Leu Val Val Gly Arg Asn Ile Gly
 355 360 365
 Leu Met Thr Met Glu Leu Phe Thr Pro Ala Arg Asp Val Leu Ala Gln
 370 375 380
 Arg Thr Leu Gly Trp Val Ala Arg
 385 390

<210> 272
 <211> 441
 <212> PRT
 <213> E. Coli

<400> 272

Met	Ser	Glu	Ile	Ser	Arg	Gln	Glu	Phe	Gln	Arg	Arg	Arg	Gln	Ala	Leu
1						5			10				15		
Val															
Val	Glu	Gln	Met	Gln	Pro	Gly	Ser	Ala	Ala	Leu	Ile	Phe	Ala	Ala	Pro
											20		25		30
Glu	Val	Thr	Arg	Ser	Ala	Asp	Ser	Glu	Tyr	Pro	Tyr	Arg	Gln	Asn	Ser
											35		40		45
Asp	Phe	Trp	Tyr	Phe	Thr	Gly	Phe	Asn	Glu	Pro	Glu	Ala	Val	Leu	Val
											50		55		60
Leu	Ile	Lys	Ser	Asp	Asp	Thr	His	Asn	His	Ser	Val	Leu	Phe	Asn	Arg
											65		70		75
Val	Arg	Asp	Leu	Thr	Ala	Glu	Ile	Trp	Phe	Gly	Arg	Arg	Leu	Gly	Gln
											85		90		95
Asp	Ala	Ala	Pro	Glu	Lys	Leu	Gly	Val	Asp	Arg	Ala	Leu	Ala	Phe	Ser
											100		105		110
Glu	Ile	Asn	Gln	Gln	Leu	Tyr	Gln	Leu	Leu	Asn	Gly	Leu	Asp	Val	Val
											115		120		125
Tyr	His	Ala	Gln	Gly	Glu	Tyr	Ala	Tyr	Ala	Asp	Val	Ile	Val	Asn	Ser
											130		135		140
Ala	Leu	Glu	Lys	Leu	Arg	Lys	Gly	Ser	Arg	Gln	Asn	Leu	Thr	Ala	Pro
											145		150		155
Ala	Thr	Met	Ile	Asp	Trp	Arg	Pro	Val	Val	His	Glu	Met	Arg	Leu	Phe

	165	170	175
Lys Ser Pro Glu Glu Ile Ala Val Leu Arg Arg Ala Gly Glu Ile Thr			
180	185	190	
Ala Met Ala His Thr Arg Ala Met Glu Lys Cys Arg Pro Gly Met Phe			
195	200	205	
Glu Tyr His Leu Glu Gly Glu Ile His His Glu Phe Asn Arg His Gly			
210	215	220	
Ala Arg Tyr Pro Ser Tyr Asn Thr Ile Val Gly Ser Gly Glu Asn Gly			
225	230	235	240
Cys Ile Leu His Tyr Thr Glu Asn Glu Cys Glu Met Arg Asp Gly Asp			
245	250	255	
Leu Val Leu Ile Asp Ala Gly Cys Glu Tyr Lys Gly Tyr Ala Gly Asp			
260	265	270	
Ile Thr Arg Thr Phe Pro Val Asn Gly Lys Phe Thr Gln Ala Gln Arg			
275	280	285	
Glu Ile Tyr Asp Ile Val Leu Glu Ser Leu Glu Thr Ser Leu Arg Leu			
290	295	300	
Tyr Arg Pro Gly Thr Ser Ile Leu Glu Val Thr Gly Glu Val Val Arg			
305	310	315	320
Ile Met Val Ser Gly Leu Val Lys Leu Gly Ile Leu Lys Gly Asp Val			
325	330	335	
Asp Glu Leu Ile Ala Gln Asn Ala His Arg Pro Phe Phe Met His Gly			
340	345	350	
Leu Ser His Trp Leu Gly Leu Asp Val His Asp Val Gly Val Tyr Gly			
355	360	365	
Gln Asp Arg Ser Arg Ile Leu Glu Pro Gly Met Val Leu Thr Val Glu			
370	375	380	
Pro Gly Leu Tyr Ile Ala Pro Asp Ala Glu Val Pro Glu Gln Tyr Arg			
385	390	395	400
Gly Ile Gly Ile Arg Ile Glu Asp Asp Ile Val Ile Thr Glu Thr Gly			
405	410	415	
Asn Glu Asn Leu Thr Ala Ser Val Val Lys Lys Pro Glu Glu Ile Glu			
420	425	430	
Ala Leu Met Val Ala Ala Arg Lys Gln			
435	440		

<210> 273

<211> 194

<212> PRT

<213> E. Coli

<400> 273

Met Leu Met Ser Ile Gln Asn Glu Met Pro Gly Tyr Asn Glu Met Asn			
1	5	10	15
Gln Tyr Leu Asn Gln Gln Gly Thr Gly Leu Thr Pro Ala Glu Met His			
20	25	30	
Gly Leu Ile Ser Gly Met Ile Cys Gly Gly Asn Asp Asp Ser Ser Trp			
35	40	45	
Leu Pro Leu Leu His Asp Leu Thr Asn Glu Gly Met Ala Phe Gly His			
50	55	60	
Glu Leu Ala Gln Ala Leu Arg Lys Met His Ser Ala Thr Ser Asp Ala			
65	70	75	80
Leu Gln Asp Asp Gly Phe Leu Phe Gln Leu Tyr Leu Pro Asp Gly Asp			
85	90	95	
Asp Val Ser Val Phe Asp Arg Ala Asp Ala Leu Ala Gly Trp Val Asn			
100	105	110	

His Phe Leu Leu Gly Leu Gly Val Thr Gln Pro Lys Leu Asp Lys Val
 115 120 125
 Thr Gly Glu Thr Gly Glu Ala Ile Asp Asp Leu Arg Asn Ile Ala Gln
 130 135 140
 Leu Gly Tyr Asp Glu Asp Glu Asp Gln Glu Glu Leu Glu Met Ser Leu
 145 150 155 160
 Glu Glu Ile Ile Glu Tyr Val Arg Val Ala Ala Leu Leu Cys His Asp
 165 170 175
 Thr Phe Thr His Pro Gln Pro Thr Ala Pro Glu Val Gln Lys Pro Thr
 180 185 190
 Leu His

<210> 274
 <211> 120
 <212> PRT
 <213> E. Coli

..<400> 274
 Met Leu Lys Leu Phe Ala Lys Tyr Thr Ser Ile Gly Val Leu Asn Thr
 1 5 10 15
 Leu Ile His Trp Val Val Phe Gly Val Cys Ile Tyr Val Ala His Thr
 20 25 30
 Asn Gln Ala Leu Ala Asn Phe Ala Gly Phe Val Val Ala Val Ser Phe
 35 40 45
 Ser Phe Phe Ala Asn Ala Lys Phe Thr Phe Lys Ala Ser Thr Thr Thr
 50 55 60
 Met Arg Tyr Met Leu Tyr Val Gly Phe Met Gly Thr Leu Ser Ala Thr
 65 70 75 80
 Val Gly Trp Ala Ala Asp Arg Cys Ala Leu Pro Pro Met Ile Thr Leu
 85 90 95
 Val Thr Phe Ser Ala Ile Ser Leu Val Cys Gly Phe Val Tyr Ser Lys
 100 105 110
 Phe Ile Val Phe Arg Asp Ala Lys
 115 120

<210> 275
 <211> 306
 <212> PRT
 <213> E. Coli

<400> 275
 Met Lys Ile Ser Leu Val Val Pro Val Phe Asn Glu Glu Glu Ala Ile
 1 5 10 15
 Pro Ile Phe Tyr Lys Thr Val Arg Glu Phe Glu Glu Leu Lys Ser Tyr
 20 25 30
 Glu Val Glu Ile Val Phe Ile Asn Asp Gly Ser Lys Asp Ala Thr Glu
 35 40 45
 Ser Ile Ile Asn Ala Leu Ala Val Ser Asp Pro Leu Val Val Pro Leu
 50 55 60
 Ser Phe Thr Arg Asn Phe Gly Lys Glu Pro Ala Leu Phe Ala Gly Leu
 65 70 75 80
 Asp His Ala Thr Gly Asp Ala Ile Ile Pro Ile Asp Val Asp Leu Gln
 85 90 95
 Asp Pro Ile Glu Val Ile Pro His Leu Ile Glu Lys Trp Gln Ala Gly
 100 105 110

Ala Asp Met Val Leu Ala Lys Arg Ser Asp Arg Ser Thr Asp Gly Arg
 115 120 125
 Leu Lys Arg Lys Thr Ala Glu Trp Phe Tyr Lys Leu His Asn Lys Ile
 130 135 140
 Ser Asn Pro Lys Ile Glu Glu Asn Val Gly Asp Phe Arg Leu Met Ser
 145 150 155 160
 Arg Asp Val Val Glu Asn Ile Lys Leu Met Pro Glu Arg Asn Leu Phe
 165 170 175
 Met Lys Gly Ile Leu Ser Trp Val Gly Gly Lys Thr Asp Ile Val Glu
 180 185 190
 Tyr Val Arg Ala Glu Arg Ile Ala Gly Asp Thr Lys Phe Asn Gly Trp
 195 200 205
 Lys Leu Trp Asn Leu Ala Leu Glu Gly Ile Thr Ser Phe Ser Thr Phe
 210 215 220
 Pro Leu Arg Ile Trp Thr Tyr Ile Gly Leu Val Val Ala Ser Val Ala
 225 230 235 240
 Phe Ile Tyr Gly Ala Trp Met Ile Leu Asp Thr Ile Ile Phe Gly Asn
 245 250 255
 Ala Val Arg Gly Tyr Pro Ser Leu Leu Val Ser Ile Leu Phe Leu Gly
 260 265 270
 Gly Ile Gln Met Ile Gly Ile Gly Val Leu Gly Glu Tyr Ile Gly Arg
 275 280 285
 Thr Tyr Ile Glu Thr Lys Lys Arg Pro Lys Tyr Ile Ile Lys Arg Val
 290 295 300
 Lys Lys
 305

<210> 276
 <211> 443
 <212> PRT
 <213> E. Coli

<400> 276
 Met Asn Lys Ala Ile Lys Val Ser Leu Tyr Ile Ser Phe Val Leu Ile
 1 5 10 15
 Ile Cys Ala Leu Ser Lys Asn Ile Met Met Leu Asn Thr Ser Asp Phe
 20 25 30
 Gly Arg Ala Ile Lys Pro Leu Ile Glu Asp Ile Pro Ala Phe Thr Tyr
 35 40 45
 Asp Leu Pro Leu Leu Tyr Lys Leu Lys Gly His Ile Asp Ser Ile Asp
 50 55 60
 Ser Tyr Glu Tyr Ile Ser Ser Tyr Ser Tyr Ile Leu Tyr Thr Tyr Val
 65 70 75 80
 Leu Phe Ile Ser Ile Phe Thr Glu Tyr Leu Asp Ala Arg Val Leu Ser
 85 90 95
 Leu Phe Leu Lys Val Ile Tyr Ile Tyr Ser Leu Tyr Ala Ile Phe Thr
 100 105 110
 Ser Tyr Ile Lys Thr Glu Arg Tyr Val Thr Leu Phe Thr Phe Phe Ile
 115 120 125
 Leu Ala Phe Leu Met Cys Ser Ser Ser Thr Leu Ser Met Phe Ala Ser
 130 135 140
 Phe Tyr Gln Glu Gln Ile Val Ile Ile Phe Leu Pro Phe Leu Val Tyr
 145 150 155 160
 Ser Leu Thr Cys Lys Asn Asn Lys Ser Met Leu Leu Leu Phe Phe Ser
 165 170 175
 Leu Leu Ile Ile Ser Thr Ala Lys Asn Gln Phe Ile Leu Thr Pro Leu

	180	185	190
Ile Val Tyr Ser Tyr Tyr Ile Phe Phe Asp Arg His Lys Leu Ile Ile			
195	200	205	
Lys Ser Val Ile Cys Val Val Cys Leu Leu Ala Ser Ile Phe Ala Ile			
210	215	220	
Ser Tyr Ser Lys Gly Val Val Glu Leu Asn Lys Tyr His Ala Thr Tyr			
225	230	235	240
Phe Gly Ser Tyr Leu Tyr Met Lys Asn Asn Gly Tyr Lys Met Pro Ser			
245	250	255	
Tyr Val Asp Asp Lys Cys Val Gly Leu Asp Ala Trp Gly Asn Lys Phe			
260	265	270	
Asp Ile Ser Phe Gly Ala Thr Pro Thr Glu Val Gly Thr Glu Cys Phe			
275	280	285	
Glu Ser His Lys Asp Glu Thr Phe Ser Asn Ala Leu Phe Leu Leu Val			
290	295	300	
Ser Lys Pro Ser Thr Ile Phe Lys Leu Pro Phe Asp Asp Gly Val Met			
305	310	315	320
Ser Gln Tyr Lys Glu Asn Tyr Phe His Val Tyr Lys Lys Leu His Val			
325	330	335	
Ile Tyr Gly Glu Ser Asn Ile Leu Thr Thr Ile Thr Asn Ile Lys Asp			
340	345	350	
Asn Ile Phe Lys Asn Ile Arg Phe Ile Ser Leu Leu Leu Phe Phe Ile			
355	360	365	
Ala Ser Ile Phe Ile Arg Asn Asn Lys Ile Lys Ala Ser Leu Phe Val			
370	375	380	
Val Ser Leu Phe Gly Ile Ser Gln Phe Tyr Val Ser Phe Phe Gly Glu			
385	390	395	400
Gly Tyr Arg Asp Leu Ser Lys His Leu Phe Gly Met Tyr Phe Ser Phe			
405	410	415	
Asp Leu Cys Leu Tyr Ile Thr Val Val Phe Leu Ile Tyr Lys Ile Ile			
420	425	430	
Gln Arg Asn Gln Asp Asn Ser Asp Val Lys His			
435	440		

<210> 277
 <211> 82
 <212> PRT
 <213> E. Coli

<400> 277
 Met Gly Ile Leu Ser Trp Ile Ile Phe Gly Leu Ile Ala Gly Ile Leu
 1 5 10 15
 Ala Lys Trp Ile Met Pro Gly Lys Asp Gly Gly Gly Phe Phe Met Thr
 20 25 30
 Ile Leu Leu Gly Ile Val Gly Ala Val Val Gly Gly Trp Ile Ser Thr
 35 40 45
 Leu Phe Gly Phe Gly Lys Val Asp Gly Phe Asn Phe Gly Ser Phe Val
 50 55 60
 Val Ala Val Ile Gly Ala Ile Val Val Leu Phe Ile Tyr Arg Lys Ile
 65 70 75 80
 Lys Ser

<210> 278

<211> 60
<212> PRT
<213> E. Coli

<400> 278
Met Gly Lys Ala Thr Tyr Thr Val Thr Val Thr Asn Asn Ser Asn Gly
1 5 10 15
Val Ser Val Asp Tyr Glu Thr Glu Thr Pro Met Thr Leu Leu Val Pro
20 25 30
Glu Val Ala Ala Glu Val Ile Lys Asp Leu Val Asn Thr Val Arg Ser
35 40 45
Tyr Asp Thr Glu Asn Glu His Asp Val Cys Gly Trp
50 55 60

<210> 279
<211> 119
<212> PRT
<213> E. Coli

<400> 279
Met Leu Gln Ile Pro Gln Asn Tyr Ile His Thr Arg Ser Thr Pro Phe
1 5 10 15
Trp Asn Lys Gln Thr Ala Pro Ala Gly Ile Phe Glu Arg His Leu Asp
20 25 30
Lys Gly Thr Arg Pro Gly Val Tyr Pro Arg Leu Ser Val Met His Gly
35 40 45
Ala Val Lys Tyr Leu Gly Tyr Ala Asp Glu His Ser Ala Glu Pro Asp
50 55 60
Gln Val Ile Leu Ile Glu Ala Gly Gln Phe Ala Val Phe Pro Pro Glu
65 70 75 80
Lys Trp His Asn Ile Glu Ala Met Thr Asp Asp Thr Tyr Phe Asn Ile
85 90 95
Asp Phe Phe Val Ala Pro Glu Val Leu Met Glu Gly Ala Gln Gln Arg
100 105 110
Lys Val Ile His Asn Gly Lys
115

<210> 280
<211> 246
<212> PRT
<213> E. Coli

<400> 280
Met Lys Phe Lys Val Ile Ala Leu Ala Ala Leu Met Gly Ile Ser Gly
1 5 10 15
Met Ala Ala Gln Ala Asn Glu Leu Pro Asp Gly Pro His Ile Val Thr
20 25 30
Ser Gly Thr Ala Ser Val Asp Ala Val Pro Asp Ile Ala Thr Leu Ala
35 40 45
Ile Glu Val Asn Val Ala Ala Lys Asp Ala Ala Thr Ala Lys Lys Gln
50 55 60
Ala Asp Glu Arg Val Ala Gln Tyr Ile Ser Phe Leu Glu Leu Asn Gln
65 70 75 80
Ile Ala Lys Lys Asp Ile Ser Ser Ala Asn Leu Arg Thr Gln Pro Asp
85 90 95

Tyr	Asp	Tyr	Gln	Asp	Gly	Lys	Ser	Ile	Leu	Lys	Gly	Tyr	Arg	Ala	Val
100								105							110
Arg	Thr	Val	Glu	Val	Thr	Leu	Arg	Gln	Leu	Asp	Lys	Leu	Asn	Ser	Leu
115								120							125
Leu	Asp	Gly	Ala	Leu	Lys	Ala	Gly	Leu	Asn	Glu	Ile	Arg	Ser	Val	Ser
130								135							140
Leu	Gly	Val	Ala	Gln	Pro	Asp	Ala	Tyr	Lys	Asp	Lys	Ala	Arg	Lys	Ala
145								150							160
Ala	Ile	Asp	Asn	Ala	Ile	His	Gln	Ala	Gln	Glu	Leu	Ala	Asn	Gly	Phe
	165							170							175
His	Arg	Lys	Leu	Gly	Pro	Val	Tyr	Ser	Val	Arg	Tyr	His	Val	Ser	Asn
	180							185							190
Tyr	Gln	Pro	Ser	Pro	Met	Val	Arg	Met	Met	Lys	Ala	Asp	Ala	Ala	Pro
	195							200							205
Val	Ser	Ala	Gln	Glu	Thr	Tyr	Glu	Gln	Ala	Ala	Ile	Gln	Phe	Asp	Asp
	210						215								220
Gln	Val	Asp	Val	Val	Phe	Gln	Leu	Glu	Pro	Val	Asp	Gln	Gln	Pro	Ala
	225				230					235					240
Lys	Thr	Pro	Ala	Ala	Gln										
	245														

<210> 281
 <211> 464
 <212> PRT
 <213> E. Coli

<400> 281															
Met	Leu	Leu	Leu	Asp	Ala	Cys	Ser	Gln	Met	Cys	Pro	Ser	Phe	Arg	Arg
1						5			10						15
Phe	Gln	Thr	Val	Phe	His	Asn	Ser	Ser	Ile	Phe	Leu	Pro	Tyr	Trp	Leu
									20	25					30
Ala	Thr	Leu	Val	Ser	Phe	Arg	Glu	Thr	Phe	Gln	Glu	Glu	Lys	Leu	Leu
								35	40						45
Thr	Met	Lys	Gly	Ser	Tyr	Lys	Ser	Arg	Trp	Val	Ile	Val	Ile	Val	Val
								50	55						60
Val	Ile	Ala	Ala	Ile	Ala	Ala	Phe	Trp	Phe	Trp	Gln	Gly	Arg	Asn	Asp
	65							70		75					80
Ser	Arg	Ser	Ala	Ala	Pro	Gly	Ala	Thr	Lys	Gln	Ala	Gln	Gln	Ser	Pro
								85		90					95
Ala	Gly	Gly	Arg	Arg	Gly	Met	Arg	Ser	Gly	Pro	Leu	Ala	Pro	Val	Gln
								100	105						110
Ala	Ala	Thr	Ala	Val	Glu	Gln	Ala	Val	Pro	Arg	Tyr	Leu	Thr	Gly	Leu
								115	120						125
Gly	Thr	Ile	Thr	Ala	Ala	Asn	Thr	Val	Thr	Val	Arg	Ser	Arg	Val	Asp
								130	135						140
Gly	Gln	Leu	Ile	Ala	Leu	His	Phe	Gln	Glu	Gly	Gln	Gln	Val	Lys	Ala
	145							150		155					160
Gly	Asp	Leu	Leu	Ala	Glu	Ile	Asp	Pro	Ser	Gln	Phe	Lys	Val	Ala	Leu
								165		170					175
Ala	Gln	Ala	Gln	Gly	Gln	Leu	Ala	Lys	Asp	Lys	Ala	Thr	Leu	Ala	Asn
								180		185					190
Ala	Arg	Arg	Asp	Leu	Ala	Arg	Tyr	Gln	Gln	Leu	Ala	Lys	Thr	Asn	Leu
	195							200							205
Val	Ser	Arg	Gln	Glu	Leu	Asp	Ala	Gln	Gln	Ala	Leu	Val	Ser	Glu	Thr
	210							215							220
Glu	Gly	Thr	Ile	Lys	Ala	Asp	Glu	Ala	Ser	Val	Ala	Ser	Ala	Gln	Leu

225	230	235	240												
Gln	Leu	Asp	Trp	Ser	Arg	Ile	Thr	Ala	Pro	Val	Asp	Gly	Arg	Val	Gly
245															255
Leu	Lys	Gln	Val	Asp	Val	Gly	Asn	Gln	Ile	Ser	Ser	Gly	Asp	Thr	Thr
260															270
Gly	Ile	Val	Val	Ile	Thr	Gln	Thr	His	Pro	Ile	Asp	Leu	Val	Phe	Thr
275															285
Leu	Pro	Glu	Ser	Asp	Ile	Ala	Thr	Val	Val	Gln	Ala	Gln	Lys	Ala	Gly
290															300
Lys	Pro	Leu	Val	Val	Glu	Ala	Trp	Asp	Arg	Thr	Asn	Ser	Lys	Lys	Leu
305															320
Ser	Glu	Gly	Thr	Leu	Leu	Ser	Leu	Asp	Asn	Gln	Ile	Asp	Ala	Thr	Thr
325															335
Gly	Thr	Ile	Lys	Val	Lys	Ala	Arg	Phe	Asn	Asn	Gln	Asp	Asp	Ala	Leu
340															350
Phe	Pro	Asn	Gln	Phe	Val	Asn	Ala	Arg	Met	Leu	Val	Asp	Thr	Glu	Gln
355															365
Asn	Ala	Val	Val	Ile	Pro	Thr	Ala	Ala	Leu	Gln	Met	Gly	Asn	Glu	Gly
370															380
His	Phe	Val	Trp	Val	Leu	Asn	Ser	Glu	Asn	Lys	Val	Ser	Lys	His	Leu
385															400
Val	Thr	Pro	Gly	Ile	Gln	Asp	Ser	Gln	Lys	Val	Val	Ile	Arg	Ala	Gly
405															415
Ile	Ser	Ala	Gly	Asp	Arg	Val	Val	Thr	Asp	Gly	Ile	Asp	Arg	Leu	Thr
420															430
Glu	Gly	Ala	Lys	Val	Glu	Val	Val	Glu	Ala	Gln	Ser	Ala	Thr	Thr	Pro
435															445
Glu	Glu	Lys	Ala	Thr	Ser	Arg	Glu	Tyr	Ala	Lys	Lys	Gly	Ala	Arg	Ser
450															460

<210> 282

<211> 1040

<212> PRT

<213> E. Coli

<400> 282

Met	Gln	Val	Leu	Pro	Pro	Ser	Ser	Thr	Gly	Gly	Pro	Ser	Arg	Leu	Phe
1															15
Ile	Met	Arg	Pro	Val	Ala	Thr	Thr	Leu	Leu	Met	Val	Ala	Ile	Leu	Leu
															30
Ala	Gly	Ile	Ile	Gly	Tyr	Arg	Ala	Leu	Pro	Val	Ser	Ala	Leu	Pro	Glu
															45
Val	Asp	Tyr	Pro	Thr	Ile	Gln	Val	Val	Thr	Leu	Tyr	Pro	Gly	Ala	Ser
															55
															60
Pro	Asp	Val	Met	Thr	Ser	Ala	Val	Thr	Ala	Pro	Leu	Glu	Arg	Gln	Phe
															75
															80
Gly	Gln	Met	Ser	Gly	Leu	Lys	Gln	Met	Ser	Ser	Gln	Ser	Ser	Gly	Gly
															95
Ala	Ser	Val	Ile	Thr	Leu	Gln	Phe	Gln	Leu	Thr	Leu	Pro	Leu	Asp	Val
															105
															110
Ala	Glu	Gln	Glu	Val	Gln	Ala	Ala	Ile	Asn	Ala	Ala	Thr	Asn	Leu	Leu
															125
Pro	Ser	Asp	Leu	Pro	Asn	Pro	Pro	Val	Tyr	Ser	Lys	Val	Asn	Pro	Ala
															135
															140
Asp	Pro	Pro	Ile	Met	Thr	Leu	Ala	Val	Thr	Ser	Thr	Ala	Met	Pro	Met
															155
															160
145															

Thr Gln Val Glu Asp Met Val Glu Thr Arg Val Ala Gln Lys Ile Ser
 165 170 175
 Gln Ile Ser Gly Val Gly Leu Val Thr Leu Ser Gly Gly Gln Arg Pro
 180 185 190
 Ala Val Arg Val Lys Leu Asn Ala Gln Ala Ile Ala Ala Leu Gly Leu
 195 200 205
 Thr Ser Glu Thr Val Arg Thr Ala Ile Thr Gly Ala Asn Val Asn Ser
 210 215 220
 Ala Lys Gly Ser Leu Asp Gly Pro Ser Arg Ala Val Thr Leu Ser Ala
 225 230 235 240
 Asn Asp Gln Met Gln Ser Ala Glu Glu Tyr Arg Gln Leu Ile Ile Ala
 245 250 255
 Tyr Gln Asn Gly Ala Pro Ile Arg Leu Gly Asp Val Ala Thr Val Glu
 260 265 270
 Gln Gly Ala Glu Asn Ser Trp Leu Gly Ala Trp Ala Asn Lys Glu Gln
 275 280 285
 Ala Ile Val Met Asn Val Gln Arg Gln Pro Gly Ala Asn Ile Ile Ser
 290 295 300
 Thr Ala Asp Ser Ile Arg Gln Met Leu Pro Gln Leu Thr Glu Ser Leu
 305 310 315 320
 Pro Lys Ser Val Lys Val Thr Val Leu Ser Asp Arg Thr Thr Asn Ile
 325 330 335
 Arg Ala Ser Val Asp Asp Thr Gln Phe Glu Leu Met Met Ala Ile Ala
 340 345 350
 Leu Val Val Met Ile Ile Tyr Leu Phe Leu Arg Asn Ile Pro Ala Thr
 355 360 365
 Ile Ile Pro Gly Val Ala Val Pro Leu Ser Leu Ile Gly Thr Phe Ala
 370 375 380
 Val Met Val Phe Leu Asp Phe Ser Ile Asn Asn Leu Thr Leu Met Ala
 385 390 395 400
 Leu Thr Ile Ala Thr Gly Phe Val Val Asp Asp Ala Ile Val Val Ile
 405 410 415
 Glu Asn Ile Ser Arg Tyr Ile Glu Lys Gly Glu Lys Pro Leu Ala Ala
 420 425 430
 Ala Leu Lys Gly Ala Gly Glu Ile Gly Phe Thr Ile Ile Ser Leu Thr
 435 440 445
 Phe Ser Leu Ile Ala Val Leu Ile Pro Leu Leu Phe Met Gly Asp Ile
 450 455 460
 Val Gly Arg Leu Phe Arg Glu Phe Ala Ile Thr Leu Ala Val Ala Ile
 465 470 475 480
 Leu Ile Ser Ala Val Val Ser Leu Thr Leu Thr Pro Met Met Cys Ala
 485 490 495
 Arg Met Leu Ser Gln Glu Ser Leu Arg Lys Gln Asn Arg Phe Ser Arg
 500 505 510
 Ala Ser Glu Lys Met Phe Asp Arg Ile Ile Ala Ala Tyr Gly Arg Gly
 515 520 525
 Leu Ala Lys Val Leu Asn His Pro Trp Leu Thr Leu Ser Val Ala Leu
 530 535 540
 Ser Thr Leu Leu Leu Ser Val Leu Leu Trp Val Phe Ile Pro Lys Gly
 545 550 555 560
 Phe Phe Pro Val Gln Asp Asn Gly Ile Ile Gln Gly Thr Leu Gln Ala
 565 570 575
 Pro Gln Ser Ser Ser Phe Ala Asn Met Ala Gln Arg Gln Arg Gln Val
 580 585 590
 Ala Asp Val Ile Leu Gln Asp Pro Ala Val Gln Ser Leu Thr Ser Phe
 595 600 605
 Val Gly Val Asp Gly Thr Asn Pro Ser Leu Asn Ser Ala Arg Leu Gln

610	615	620
Ile Asn Leu Lys Pro Leu Asp Glu Arg Asp Asp Arg Val Gln Lys Val		
625	630	635
Ile Ala Arg Leu Gln Thr Ala Val Asp Lys Val Pro Gly Val Asp Leu		640
645	650	655
Phe Leu Gln Pro Thr Gln Asp Leu Thr Ile Asp Thr Gln Val Ser Arg		
660	665	670
Thr Gln Tyr Gln Phe Thr Leu Gln Ala Thr Ser Leu Asp Ala Leu Ser		
675	680	685
Thr Trp Val Pro Gln Leu Met Glu Lys Leu Gln Gln Leu Pro Gln Leu		
690	695	700
Ser Asp Val Ser Ser Asp Trp Gln Asp Lys Gly Leu Val Ala Tyr Val		
705	710	715
Asn Val Asp Arg Asp Ser Ala Ser Arg Leu Gly Ile Ser Met Ala Asp		720
725	730	735
Val Asp Asn Ala Leu Tyr Asn Ala Phe Gly Gln Arg Leu Ile Ser Thr		
740	745	750
Ile Tyr Thr Gln Ala Asn Gln Tyr Arg Val Val Leu Glu His Asn Thr		
755	760	765
Glu Asn Thr Pro Gly Leu Ala Ala Leu Asp Thr Ile Arg Leu Thr Ser		
770	775	780
Ser Asp Gly Gly Val Val Pro Leu Ser Ser Ile Ala Lys Ile Glu Gln		
785	790	795
Arg Phe Ala Pro Leu Ser Ile Asn His Leu Asp Gln Phe Pro Val Thr		800
805	810	815
Thr Ile Ser Phe Asn Val Pro Asp Asn Tyr Ser Leu Gly Asp Ala Val		
820	825	830
Gln Ala Ile Met Asp Thr Glu Lys Thr Leu Asn Leu Pro Val Asp Ile		
835	840	845
Thr Thr Gln Phe Gln Gly Ser Thr Leu Ala Phe Gln Ser Ala Leu Gly		
850	855	860
Ser Thr Val Trp Leu Ile Val Ala Ala Val Val Ala Met Tyr Ile Val		
865	870	875
Leu Gly Ile Leu Tyr Glu Ser Phe Ile His Pro Ile Thr Ile Leu Ser		
885	890	895
Thr Leu Pro Thr Ala Gly Val Gly Ala Leu Leu Ala Leu Ile Ala		
900	905	910
Gly Ser Glu Leu Asp Val Ile Ala Ile Ile Gly Ile Ile Leu Leu Ile		
915	920	925
Gly Ile Val Lys Lys Asn Ala Ile Met Met Ile Asp Phe Ala Leu Ala		
930	935	940
Ala Glu Arg Glu Gln Gly Met Ser Pro Arg Glu Ala Ile Tyr Gln Ala		
945	950	955
Cys Leu Leu Arg Phe Arg Pro Ile Leu Met Thr Thr Leu Ala Ala Leu		960
965	970	975
Leu Gly Ala Leu Pro Leu Met Leu Ser Thr Gly Val Gly Ala Glu Leu		
980	985	990
Arg Arg Pro Leu Gly Ile Gly Met Val Gly Gly Leu Ile Val Ser Gln		
995	1000	1005
Val Leu Thr Leu Phe Thr Thr Pro Val Ile Tyr Leu Leu Phe Asp Arg		
1010	1015	1020
Leu Ala Leu Trp Thr Lys Ser Arg Phe Ala Arg His Glu Glu Glu Ala		
1025	1030	1035
		1040

<210> 283

<211> 1025

<212> PRT

<213> E. Coli

<400> 283

Met Lys Phe Phe Ala Leu Phe Ile Tyr Arg Pro Val Ala Thr Ile Leu
1 5 10 15
Leu Ser Val Ala Ile Thr Leu Cys Gly Ile Leu Gly Phe Arg Met Leu
20 25 30
Pro Val Ala Pro Leu Pro Gln Val Asp Phe Pro Val Ile Ile Val Ser
35 40 45
Ala Ser Leu Pro Gly Ala Ser Pro Glu Thr Met Ala Ser Ser Val Ala
50 55 60
Thr Pro Leu Glu Arg Ser Leu Gly Arg Ile Ala Gly Val Ser Glu Met
65 70 75 80
Thr Ser Ser Ser Leu Gly Ser Thr Arg Ile Ile Leu Gln Phe Asp
85 90 95
Phe Asp Arg Asp Ile Asn Gly Ala Ala Arg Asp Val Gln Ala Ala Ile
100 105 110
Asn Ala Ala Gln Ser Leu Leu Pro Ser Gly Met Pro Ser Arg Pro Thr
115 120 125
Tyr Arg Lys Ala Asn Pro Ser Asp Ala Pro Ile Met Ile Leu Thr Leu
130 135 140
Thr Ser Asp Thr Tyr Ser Gln Gly Glu Leu Tyr Asp Phe Ala Ser Thr
145 150 155 160
Gln Leu Ala Pro Thr Ile Ser Gln Ile Asp Gly Val Gly Asp Val Asp
165 170 175
Val Gly Gly Ser Ser Leu Pro Ala Val Arg Val Gly Leu Asn Pro Gln
180 185 190
Ala Leu Phe Asn Gln Gly Val Ser Leu Asp Asp Val Arg Thr Ala Val
195 200 205
Ser Asn Ala Asn Val Arg Lys Pro Gln Gly Ala Leu Glu Asp Gly Thr
210 215 220
His Arg Trp Gln Ile Gln Thr Asn Asp Glu Leu Lys Thr Ala Ala Glu
225 230 235 240
Tyr Gln Pro Leu Ile Ile His Tyr Asn Asn Gly Gly Ala Val Arg Leu
245 250 255
Gly Asp Val Ala Thr Val Thr Asp Ser Val Gln Asp Val Arg Asn Ala
260 265 270
Gly Met Thr Asn Ala Lys Pro Ala Ile Leu Leu Met Ile Arg Lys Leu
275 280 285
Pro Glu Ala Asn Ile Ile Gln Thr Val Asp Ser Ile Arg Ala Lys Leu
290 295 300
Pro Glu Leu Gln Glu Thr Ile Pro Ala Ala Ile Asp Leu Gln Ile Ala
305 310 315 320
Gln Asp Arg Ser Pro Thr Ile Arg Ala Ser Leu Glu Glu Val Glu Gln
325 330 335
Thr Leu Ile Ile Ser Val Ala Leu Val Ile Leu Val Val Phe Leu Phe
340 345 350
Leu Arg Ser Gly Arg Ala Thr Ile Ile Pro Ala Val Ser Val Pro Val
355 360 365
Ser Leu Ile Gly Thr Phe Ala Ala Met Tyr Leu Cys Gly Phe Ser Leu
370 375 380
Asn Asn Leu Ser Leu Met Ala Leu Thr Ile Ala Thr Gly Phe Val Val
385 390 395 400
Asp Asp Ala Ile Val Val Leu Glu Asn Ile Ala Arg His Leu Glu Ala
405 410 415
Gly Met Lys Pro Leu Gln Ala Ala Leu Gln Gly Thr Arg Glu Val Gly

420	425	430													
Phe	Thr	Val	Leu	Ser	Met	Ser	Leu	Ser	Leu	Val	Ala	Val	Phe	Leu	Pro
435							440						445		
Leu	Leu	Leu	Met	Gly	Gly	Leu	Pro	Gly	Arg	Leu	Leu	Arg	Glu	Phe	Ala
450							455						460		
Val	Thr	Leu	Ser	Val	Ala	Ile	Gly	Ile	Ser	Leu	Leu	Val	Ser	Leu	Thr
465							470						475		
Leu	Thr	Pro	Met	Met	Cys	Gly	Trp	Met	Leu	Lys	Ala	Ser	Lys	Pro	Arg
								485					490		
Glu	Gln	Lys	Arg	Leu	Arg	Gly	Phe	Gly	Arg	Met	Leu	Val	Ala	Leu	Gln
								500					505		
Gln	Gly	Tyr	Gly	Lys	Ser	Leu	Lys	Trp	Val	Leu	Asn	His	Thr	Arg	Leu
								515					520		
Val	Gly	Val	Val	Leu	Leu	Gly	Thr	Ile	Ala	Leu	Asn	Ile	Trp	Leu	Tyr
								530					535		
Ile	Ser	Ile	Pro	Lys	Thr	Phe	Phe	Pro	Glu	Gln	Asp	Thr	Gly	Val	Leu
								545					550		
Met	Gly	Gly	Ile	Gln	Ala	Asp	Gln	Ser	Ile	Ser	Phe	Gln	Ala	Met	Arg
								565					570		
Gly	Lys	Leu	Gln	Asp	Phe	Met	Lys	Ile	Ile	Arg	Asp	Asp	Pro	Ala	Val
								580					585		
Asp	Asn	Val	Thr	Gly	Phe	Thr	Gly	Gly	Ser	Arg	Val	Asn	Ser	Gly	Met
								595					600		
Met	Phe	Ile	Thr	Leu	Lys	Pro	Arg	Asp	Glu	Arg	Ser	Glu	Thr	Ala	Gln
								610					615		
Gln	Ile	Ile	Asp	Arg	Leu	Arg	Val	Lys	Leu	Ala	Lys	Glu	Pro	Gly	Ala
								625					630		
Asn	Leu	Phe	Leu	Met	Ala	Val	Gln	Asp	Ile	Arg	Val	Gly	Arg	Gln	
								645					650		
Ser	Asn	Ala	Ser	Tyr	Gln	Tyr	Thr	Leu	Leu	Ser	Asp	Asp	Leu	Ala	Ala
								660					665		
Leu	Arg	Glu	Trp	Glu	Pro	Lys	Ile	Arg	Lys	Lys	Leu	Ala	Thr	Leu	Pro
								675					680		
Glu	Leu	Ala	Asp	Val	Asn	Ser	Asp	Gln	Gln	Asp	Asn	Gly	Ala	Glu	Met
								690					695		
Asn	Leu	Val	Tyr	Asp	Arg	Asp	Thr	Met	Ala	Arg	Leu	Gly	Ile	Asp	Val
								705					710		
Gln	Ala	Ala	Asn	Ser	Leu	Leu	Asn	Asn	Ala	Phe	Gly	Gln	Arg	Gln	Ile
								725					730		
Ser	Thr	Ile	Tyr	Gln	Pro	Met	Asn	Gln	Tyr	Lys	Val	Val	Met	Glu	Val
								740					745		
Asp	Pro	Arg	Tyr	Thr	Gln	Asp	Ile	Ser	Ala	Leu	Glu	Lys	Met	Phe	Val
								755					760		
Ile	Asn	Asn	Glu	Gly	Lys	Ala	Ile	Pro	Leu	Ser	Tyr	Phe	Ala	Lys	Trp
								770					775		
Gln	Pro	Ala	Asn	Ala	Pro	Leu	Ser	Val	Asn	His	Gln	Gly	Leu	Ser	Ala
								785					790		
Ala	Ser	Thr	Ile	Ser	Phe	Asn	Leu	Pro	Thr	Gly	Lys	Ser	Leu	Ser	Asp
								805					810		
Ala	Ser	Ala	Ala	Ile	Asp	Arg	Ala	Met	Thr	Gln	Leu	Gly	Val	Pro	Ser
								820					825		
Thr	Val	Arg	Gly	Ser	Phe	Ala	Gly	Thr	Ala	Gln	Val	Phe	Gln	Glu	Thr
								835					840		
Met	Asn	Ser	Gln	Val	Ile	Leu	Ile	Ile	Ala	Ala	Ile	Ala	Thr	Val	Tyr
								850					855		
Ile	Val	Leu	Gly	Ile	Leu	Tyr	Glu	Ser	Tyr	Val	His	Pro	Leu	Thr	Ile
								865					870		
													875		
														880	

Leu Ser Thr Leu Pro Ser Ala Gly Val Gly Ala Leu Leu Ala Leu Glu
 885 890 895
 Leu Phe Asn Ala Pro Phe Ser Leu Ile Ala Leu Ile Gly Ile Met Leu
 900 905 910
 Leu Ile Gly Ile Val Lys Lys Asn Ala Ile Met Met Val Asp Phe Ala
 915 920 925
 Leu Glu Ala Gln Arg His Gly Asn Leu Thr Pro Gln Glu Ala Ile Phe
 930 935 940
 Gln Ala Cys Leu Leu Arg Phe Arg Pro Ile Met Met Thr Thr Leu Ala
 945 950 955 960
 Ala Leu Phe Gly Ala Leu Pro Leu Val Leu Ser Gly Gly Asp Gly Ser
 965 970 975
 Glu Leu Arg Gln Pro Leu Gly Ile Thr Ile Val Gly Gly Leu Val Met
 980 985 990
 Ser Gln Leu Leu Thr Leu Tyr Thr Thr Pro Val Val Tyr Leu Phe Phe
 995 1000 1005
 Asp Arg Leu Arg Leu Arg Phe Ser Arg Lys Pro Lys Gln Thr Val Thr
 1010 1015 1020
 Glu
 1025

<210> 284
 <211> 471
 <212> PRT
 <213> E. Coli

<400> 284
 Met Thr Asp Leu Pro Asp Ser Thr Arg Trp Gln Leu Trp Ile Val Ala
 1 5 10 15
 Phe Gly Phe Phe Met Gln Ser Leu Asp Thr Thr Ile Val Asn Thr Ala
 20 25 30
 Leu Pro Ser Met Ala Gln Ser Leu Gly Glu Ser Pro Leu His Met His
 35 40 45
 Met Val Ile Val Ser Tyr Val Leu Thr Val Ala Val Met Leu Pro Ala
 50 55 60
 Ser Gly Trp Leu Ala Asp Lys Val Gly Val Arg Asn Ile Phe Phe Thr
 65 70 75 80
 Ala Ile Val Leu Phe Thr Leu Gly Ser Leu Phe Cys Ala Leu Ser Gly
 85 90 95
 Thr Leu Asn Glu Leu Leu Ala Arg Ala Leu Gln Gly Val Gly Gly
 100 105 110
 Ala Met Met Val Pro Val Gly Arg Leu Thr Val Met Lys Ile Val Pro
 115 120 125
 Arg Glu Gln Tyr Met Ala Ala Met Thr Phe Val Thr Leu Pro Gly Gln
 130 135 140
 Val Gly Pro Leu Leu Gly Pro Ala Leu Gly Gly Leu Leu Val Glu Tyr
 145 150 155 160
 Ala Ser Trp His Trp Ile Phe Leu Ile Asn Ile Pro Val Gly Ile Ile
 165 170 175
 Gly Ala Ile Ala Thr Leu Leu Leu Met Pro Asn Tyr Thr Met Gln Thr
 180 185 190
 Arg Arg Phe Asp Leu Ser Gly Phe Leu Leu Leu Ala Val Gly Met Ala
 195 200 205
 Val Leu Thr Leu Ala Leu Asp Gly Ser Lys Gly Thr Gly Leu Ser Pro
 210 215 220
 Leu Thr Ile Ala Gly Leu Val Ala Val Gly Val Val Ala Leu Val Leu

225	230	235	240
Tyr Leu Leu His Ala Arg Asn Asn Asn Arg Ala	Leu Phe Ser	Leu Lys	
245	250	255	
Leu Phe Arg Thr Arg Thr Phe Ser	Leu Gly	Leu Ala Gly	Ser Phe Ala
260	265	270	
Gly Arg Ile Gly Ser Gly Met	Leu Pro Phe Met	Thr Pro Val	Phe Leu
275	280	285	
Gln Ile Gly Leu Gly Phe Ser	Pro Phe His Ala	Gly Leu Met	Met Met Ile
290	295	300	
Pro Met Val Leu Gly Ser Met Gly Met	Lys Arg Ile	Val Val Gln	Val
305	310	315	320
Val Asn Arg Phe Gly Tyr Arg Arg Val	Leu Val Ala	Thr Thr Leu	Gly
325	330	335	
Leu Ser Leu Val Thr Leu Leu Phe Met	Thr Thr Ala	Leu Leu Gly	Trp
340	345	350	
Tyr Tyr Val Leu Pro Phe Val	Leu Phe Leu Gln	Gly Met Val	Asn Ser
355	360	365	
Thr Arg Phe Ser Ser Met Asn	Thr Leu Thr Leu	Lys Asp Leu	Pro Asp
370	375	380	
Asn Leu Ala Ser Ser Gly Asn Ser	Leu Leu Ser Met	Ile Met Gln	Leu
385	390	395	400
Ser Met Ser Ile Gly Val Thr Ile Ala	Gly Leu Leu Leu	Gly Leu Phe	
405	410	415	
Gly Ser Gln His Val Ser Val Asp Ser	Gly Thr Thr Gln	Thr Val Phe	
420	425	430	
Met Tyr Thr Trp Leu Ser Met Ala	Leu Ile Ile Ala	Leu Pro Ala	Phe
435	440	445	
Ile Phe Ala Arg Val Pro Asn Asp Thr His	Gln Asn Val Ala	Ile Ser	
450	455	460	
Arg Arg Lys Arg Ser Ala Gln			
465	470		

<210> 285
 <211> 344
 <212> PRT
 <213> E. Coli

<400> 285			
Met Glu Ile Arg Ile Met Leu Phe Ile	Leu Met Met Met Val	Met Pro	
1	5	10	15
Val Ser Tyr Ala Ala Cys Tyr Ser	Glu Leu Ser Val Gln	His Asn Leu	
20	25	30	
Val Val Gln Gly Asp Phe Ala	Leu Thr Gln Thr Gln	Met Ala Thr Tyr	
35	40	45	
Glu His Asn Phe Asn Asp Ser Ser	Cys Val Ser Thr Asn	Thr Ile Thr	
50	55	60	
Pro Met Ser Pro Ser Asp Ile Ile	Val Gly Leu Tyr Asn Asp Thr	Ile	
65	70	75	80
Lys Leu Asn Leu His Phe Glu Trp	Thr Asn Lys Asn Asn	Ile Thr Leu	
85	90	95	
Ser Asn Asn Gln Thr Ser Phe Thr	Ser Gly Tyr Ser Val	Thr Val Thr	
100	105	110	
Pro Ala Ala Ser Asn Ala Lys Val	Asn Val Ser Ala	Gly Gly Gly	
115	120	125	
Ser Val Met Ile Asn Gly Val Ala	Thr Leu Ser Ser	Ala Ser Ser Ser	
130	135	140	

Thr Arg Gly Ser Ala Ala Val Gln Phe Leu Leu Cys Leu Leu Gly Gly
 145 150 155 160
 Lys Ser Trp Asp Ala Cys Val Asn Ser Tyr Arg Asn Ala Leu Ala Gln
 165 170 175
 Asn Ala Gly Val Tyr Ser Phe Asn Leu Thr Leu Ser Tyr Asn Pro Ile
 180 185 190
 Thr Thr Thr Cys Lys Pro Asp Asp Leu Leu Ile Thr Leu Asp Ser Ile
 195 200 205
 Pro Val Ser Gln Leu Pro Ala Thr Gly Asn Lys Ala Thr Ile Asn Ser
 210 215 220
 Lys Gln Gly Asp Ile Ile Leu Arg Cys Lys Asn Leu Leu Gly Gln Gln
 225 230 235 240
 Asn Gln Thr Ser Arg Lys Met Gln Val Tyr Leu Ser Ser Ser Asp Leu
 245 250 255
 Leu Thr Asn Ser Asn Thr Ile Leu Lys Gly Ala Glu Asp Asn Gly Val
 260 265 270
 Gly Phe Ile Leu Glu Ser Asn Gly Ser Pro Val Thr Leu Leu Asn Ile
 275 280 285
 Thr Asn Ser Ser Lys Gly Tyr Thr Asn Leu Lys Glu Val Ala Ala Lys
 290 295 300
 Ser Lys Leu Thr Asp Thr Thr Val Ser Ile Pro Ile Thr Ala Ser Tyr
 305 310 315 320
 Tyr Val Tyr Asp Thr Asn Lys Val Lys Ser Gly Ala Leu Glu Ala Thr
 325 330 335
 Ala Leu Ile Asn Val Lys Tyr Asp
 340

<210> 286
 <211> 826
 <212> PRT
 <213> E. Coli

<400> 286
 Met Leu Arg Met Thr Pro Leu Ala Ser Ala Ile Val Ala Leu Leu Leu
 1 5 10 15
 Gly Ile Glu Ala Tyr Ala Ala Glu Glu Thr Phe Asp Thr His Phe Met
 20 25 30
 Ile Gly Gly Met Lys Asp Gln Gln Val Ala Asn Ile Arg Leu Asp Asp
 35 40 45
 Asn Gln Pro Leu Pro Gly Gln Tyr Asp Ile Asp Ile Tyr Val Asn Lys
 50 55 60
 Gln Trp Arg Gly Lys Tyr Glu Ile Ile Val Lys Asp Asn Pro Gln Glu
 65 70 75 80
 Thr Cys Leu Ser Arg Glu Val Ile Lys Arg Leu Gly Ile Asn Ser Asp
 85 90 95
 Asn Phe Ala Ser Gly Lys Gln Cys Leu Thr Phe Glu Gln Leu Val Gln
 100 105 110
 Gly Gly Ser Tyr Thr Trp Asp Ile Gly Val Phe Arg Leu Asp Phe Ser
 115 120 125
 Val Pro Gln Ala Trp Val Glu Glu Leu Glu Ser Gly Tyr Val Pro Pro
 130 135 140
 Glu Asn Trp Glu Arg Gly Ile Asn Ala Phe Tyr Thr Ser Tyr Tyr Leu
 145 150 155 160
 Ser Gln Tyr Tyr Ser Asp Tyr Lys Ala Ser Gly Asn Asn Lys Ser Thr
 165 170 175
 Tyr Val Arg Phe Asn Ser Gly Leu Asn Leu Leu Gly Trp Gln Leu His

180	185	190
Ser Asp Ala Ser Phe Ser Lys	Thr Asn Asn Asn Pro	Gly Val Trp Lys
195	200	205
Ser Asn Thr Leu Tyr Leu Glu Arg Gly Phe Ala Gln	Leu Leu Gly Thr	
210	215	220
Leu Arg Val Gly Asp Met Tyr Thr Ser Ser Asp Ile Phe Asp Ser Val		
225	230	235
Arg Phe Arg Gly Val Arg Leu Phe Arg Asp Met Gln Met Leu Pro Asn		
245	250	255
Ser Lys Gln Asn Phe Thr Pro Arg Val Gln Gly Ile Ala Gln Ser Asn		
260	265	270
Ala Leu Val Thr Ile Glu Gln Asn Gly Phe Val Val Tyr Gln Lys Glu		
275	280	285
Val Pro Pro Gly Pro Phe Ala Ile Thr Asp Leu Gln Leu Ala Gly Gly		
290	295	300
Gly Ala Asp Leu Asp Val Ser Val Lys Glu Ala Asp Gly Ser Val Thr		
305	310	315
Thr Tyr Leu Val Pro Tyr Ala Ala Val Pro Asn Met Leu Gln Pro Gly		
325	330	335
Val Ser Lys Tyr Asp Leu Ala Ala Gly Arg Ser His Ile Glu Gly Ala		
340	345	350
Ser Lys Gln Ser Asp Phe Val Gln Ala Gly Tyr Gln Tyr Gly Phe Asn		
355	360	365
Asn Leu Leu Thr Leu Tyr Gly Gly Ser Met Val Ala Asn Asn Tyr Tyr		
370	375	380
Ala Phe Thr Leu Gly Ala Gly Trp Asn Thr Arg Ile Gly Ala Ile Ser		
385	390	395
Val Asp Ala Thr Lys Ser His Ser Lys Gln Asp Asn Gly Asp Val Phe		
405	410	415
Asp Gly Gln Ser Tyr Gln Ile Ala Tyr Asn Lys Phe Val Ser Gln Thr		
420	425	430
Ser Thr Arg Phe Gly Leu Ala Ala Trp Arg Tyr Ser Ser Arg Asp Tyr		
435	440	445
Arg Thr Phe Asn Asp His Val Trp Ala Asn Asn Lys Asp Asn Tyr Arg		
450	455	460
Arg Asp Glu Asn Asp Val Tyr Asp Ile Ala Asp Tyr Tyr Gln Asn Asp		
465	470	475
Phe Gly Arg Lys Asn Ser Phe Ser Ala Asn Met Ser Gln Ser Leu Pro		
485	490	495
Glu Gly Trp Gly Ser Val Ser Leu Ser Thr Leu Trp Arg Asp Tyr Trp		
500	505	510
Gly Arg Ser Gly Ser Ser Lys Asp Tyr Gln Leu Ser Tyr Ser Asn Asn		
515	520	525
Leu Arg Arg Ile Ser Tyr Thr Leu Ala Ala Ser Gln Ala Tyr Asp Glu		
530	535	540
Asn His His Glu Glu Lys Arg Phe Asn Ile Phe Ile Ser Ile Pro Phe		
545	550	555
Asp Trp Gly Asp Asp Val Ser Thr Pro Arg Arg Gln Ile Tyr Met Ser		
565	570	575
Asn Ser Thr Thr Phe Asp Asp Gln Gly Phe Ala Ser Asn Asn Thr Gly		
580	585	590
Leu Ser Gly Thr Val Gly Ser Arg Asp Gln Phe Asn Tyr Gly Val Asn		
595	600	605
Leu Ser His Gln His Gln Gly Asn Glu Thr Thr Ala Gly Ala Asn Leu		
610	615	620
Thr Trp Asn Ala Pro Val Ala Thr Val Asn Gly Ser Tyr Ser Gln Ser		
625	630	635
		640

Ser Thr Tyr Arg Gln Ala Gly Ala Ser Val Ser Gly Gly Ile Val Ala
 645 650 655
 Trp Ser Gly Gly Val Asn Leu Ala Asn Arg Leu Ser Glu Thr Phe Ala
 660 665 670
 Val Met Asn Ala Pro Gly Ile Lys Asp Ala Tyr Val Asn Gly Gln Lys
 675 680 685
 Tyr Arg Thr Thr Asn Arg Asn Gly Val Val Ile Tyr Asp Gly Met Thr
 690 695 700
 Pro Tyr Arg Glu Asn His Leu Met Leu Asp Val Ser Gln Ser Asp Ser
 705 710 715 720
 Glu Ala Glu Leu Arg Gly Asn Arg Lys Ile Ala Ala Pro Tyr Arg Gly
 725 730 735
 Ala Val Val Leu Val Asn Phe Asp Thr Asp Gln Arg Lys Pro Trp Phe
 740 745 750
 Ile Lys Ala Leu Arg Ala Asp Gly Gln Ser Leu Thr Phe Gly Tyr Glu
 755 760 765
 Val Asn Asp Ile His Gly His Asn Ile Gly Val Val Gly Gln Gly Ser
 770 775 780
 Gln Leu Phe Ile Arg Thr Asn Glu Val Pro Pro Ser Val Asn Val Ala
 785 790 795 800
 Ile Asp Lys Gln Gln Gly Leu Ser Cys Thr Ile Thr Phe Gly Lys Glu
 805 810 815
 Ile Asp Glu Ser Arg Asn Tyr Ile Cys Gln
 820 825

<210> 287
 <211> 239
 <212> PRT
 <213> E. Coli

<400> 287
 Met Ala Ala Ile Pro Trp Arg Pro Phe Asn Leu Arg Gly Ile Lys Met
 1 5 10 15
 Lys Gly Leu Leu Ser Leu Leu Ile Phe Ser Met Val Leu Pro Ala His
 20 25 30
 Ala Gly Ile Val Ile Tyr Gly Thr Arg Ile Ile Tyr Pro Ala Glu Asn
 35 40 45
 Lys Glu Val Met Val Gln Leu Met Asn Gln Gly Asn Arg Ser Ser Leu
 50 55 60
 Leu Gln Ala Trp Ile Asp Asp Gly Asp Thr Ser Leu Pro Pro Glu Lys
 65 70 75 80
 Ile Gln Val Pro Phe Met Leu Thr Pro Pro Val Ala Lys Ile Gly Ala
 85 90 95
 Asn Ser Gly Gln Gln Val Lys Ile Lys Ile Met Pro Asn Lys Leu Pro
 100 105 110
 Thr Asn Lys Glu Ser Ile Phe Tyr Leu Asn Val Leu Asp Ile Pro Pro
 115 120 125
 Asn Ser Pro Glu Gln Glu Gly Lys Asn Ala Leu Lys Phe Ala Met Gln
 130 135 140
 Asn Arg Ile Lys Leu Phe Tyr Arg Pro Ala Gly Ile Ala Pro Val Asn
 145 150 155 160
 Lys Ala Thr Phe Lys Lys Leu Leu Val Asn Arg Ser Gly Asn Gly Leu
 165 170 175
 Val Ile Lys Asn Asp Ser Ala Asn Trp Val Thr Ile Ser Asp Val Lys
 180 185 190
 Ala Asn Asn Val Lys Val Asn Tyr Glu Thr Ile Met Ile Ala Pro Leu

195	200	205
Glu Ser Gln Ser Val Asn Val Lys Ser Asn Asn Ala Asn Asn Trp His		
210	215	220
Leu Thr Ile Ile Asp Asp His Gly Asn Tyr Ile Ser Asp Lys Ile		
225	230	235

<210> 288
<211> 180
<212> PRT
<213> E. Coli

<400> 288		
Met Lys Arg Ser Ile Ile Ala Ala Val Phe Ser Ser Phe Phe Met		
1 5 10 15		
Ser Ala Gly Val Phe Ala Ala Asp Val Asp Thr Gly Thr Leu Thr Ile		
20 25 30		
Lys Gly Asn Ile Ala Glu Ser Pro Cys Lys Phe Glu Ala Gly Gly Asp		
35 40 45		
Ser Val Ser Ile Asn Met Pro Thr Val Pro Thr Ser Val Phe Glu Gly		
50 55 60		
Lys Ala Lys Tyr Ser Thr Tyr Asp Asp Ala Val Gly Val Thr Ser Ser		
65 70 75 80		
Met Leu Lys Ile Ser Cys Pro Lys Glu Val Ala Gly Val Lys Leu Ser		
85 90 95		
Leu Ile Thr Asn Asp Lys Ile Thr Gly Asn Asp Lys Ala Ile Ala Ser		
100 105 110		
Ser Asn Asp Thr Val Gly Tyr Tyr Leu Tyr Leu Gly Asp Asn Ser Asp		
115 120 125		
Val Leu Asp Val Ser Ala Pro Phe Asn Ile Glu Ser Tyr Lys Thr Ala		
130 135 140		
Glu Gly Gln Tyr Ala Ile Pro Phe Lys Ala Lys Tyr Leu Lys Leu Thr		
145 150 155 160		
Asp Asn Ser Val Gln Ser Gly Asp Val Leu Ser Ser Leu Val Met Arg		
165 170 175		
Val Ala Gln Asp		
180		

<210> 289
<211> 112
<212> PRT
<213> E. Coli

<400> 289		
Met Ser Ser Glu Arg Asp Leu Val Asn Phe Leu Gly Asp Phe Ser Met		
1 5 10 15		
Asp Val Ala Lys Ala Val Ile Ala Gly Gly Val Ala Thr Ala Ile Gly		
20 25 30		
Ser Leu Ala Ser Phe Ala Cys Val Ser Phe Gly Phe Pro Val Ile Leu		
35 40 45		
Val Gly Gly Ala Ile Leu Leu Thr Gly Ile Val Cys Thr Val Val Leu		
50 55 60		
Asn Glu Ile Asp Ala Gln Cys His Leu Ser Glu Lys Leu Lys Tyr Ala		
65 70 75 80		
Ile Arg Asp Gly Leu Lys Arg Gln Gln Glu Leu Asp Lys Trp Lys Arg		

	85		90		95	
Glu Asn Met Thr Pro Phe Met Tyr Val Leu Asn Thr Pro Pro Val Ile						
100			105		110	

<210> 290
<211> 193
<212> PRT
<213> E. Coli

<400> 290

Met Thr Asp Tyr Leu Leu Phe Val Gly Thr Val Leu Val Asn Asn						
1	5		10		15	
Phe Val Leu Val Lys Phe Leu Gly Leu Cys Pro Phe Met Gly Val Ser						
20			25		30	
Lys Lys Leu Glu Thr Ala Met Gly Met Gly Leu Ala Thr Thr Phe Val						
35			40		45	
Met Thr Leu Ala Ser Ile Cys Ala Trp Leu Ile Asp Thr Trp Ile Leu						
50			55		60	
Ile Pro Leu Asn Leu Ile Tyr Leu Arg Thr Leu Ala Phe Ile Leu Val						
65			70		75	
Ile Ala Val Val Val Gln Phe Thr Glu Met Val Val Arg Lys Thr Ser						
85			90		95	
Pro Val Leu Tyr Arg Leu Leu Gly Ile Phe Leu Pro Leu Ile Thr Thr						
100			105		110	
Asn Cys Ala Val Leu Gly Val Ala Leu Leu Asn Ile Asn Leu Gly His						
115			120		125	
Asn Phe Leu Gln Ser Ala Leu Tyr Gly Phe Ser Ala Ala Val Gly Phe						
130			135		140	
Ser Leu Val Met Val Leu Phe Ala Ala Ile Arg Glu Arg Leu Ala Val						
145			150		155	
Ala Asp Val Pro Ala Pro Phe Arg Gly Asn Ala Ile Ala Leu Ile Thr						
165			170		175	
Ala Gly Leu Met Ser Leu Ala Phe Met Gly Phe Ser Gly Leu Val Lys						
180			185		190	
Leu						

<210> 291
<211> 192
<212> PRT
<213> E. Coli

<400> 291

Met Asn Ala Ile Trp Ile Ala Val Ala Ala Val Ser Leu Leu Gly Leu						
1	5		10		15	
Ala Phe Gly Ala Ile Leu Gly Tyr Ala Ser Arg Arg Phe Ala Val Glu						
20			25		30	
Asp Asp Pro Val Val Glu Lys Ile Asp Glu Ile Leu Pro Gln Ser Gln						
35			40		45	
Cys Gly Gln Cys Gly Tyr Pro Gly Cys Arg Pro Tyr Ala Glu Ala Ile						
50			55		60	
Ser Cys Asn Gly Glu Lys Ile Asn Arg Cys Ala Pro Gly Gly Glu Ala						
65			70		75	
Val Met Leu Lys Ile Ala Glu Leu Leu Asn Val Glu Pro Gln Pro Leu						

	85	90	95												
Asp	Gly	Glu	Ala	Gln	Glu	Ile	Thr	Pro	Ala	Arg	Met	Val	Ala	Val	Ile
			100					105				110			
Asp	Glu	Asn	Asn	Cys	Ile	Gly	Cys	Thr	Lys	Cys	Ile	Gln	Ala	Cys	Pro
		115					120				125				
Val	Asp	Ala	Ile	Val	Gly	Ala	Thr	Arg	Ala	Met	His	Thr	Val	Met	Ser
		130					135			140					
Asp	Leu	Cys	Thr	Gly	Cys	Asn	Leu	Cys	Val	Asp	Pro	Cys	Pro	Thr	His
		145					150			155			160		
Cys	Ile	Ser	Leu	Gln	Pro	Val	Ala	Glu	Thr	Pro	Asp	Ser	Trp	Lys	Trp
			165					170			175				
Asp	Leu	Asn	Thr	Ile	Pro	Val	Arg	Ile	Ile	Pro	Val	Glu	His	His	Ala
			180					185			190				

<210> 292
 <211> 740
 <212> PRT
 <213> E. Coli

<400> 292

Met	Leu	Lys	Leu	Phe	Ser	Ala	Phe	Arg	Lys	Asn	Lys	Ile	Trp	Asp	Phe
1				5					10				15		
Asn	Gly	Gly	Ile	His	Pro	Pro	Glu	Met	Lys	Thr	Gln	Ser	Asn	Gly	Thr
				20					25				30		
Pro	Leu	Arg	Gln	Val	Pro	Leu	Ala	Gln	Arg	Phe	Val	Ile	Pro	Leu	Lys
			35				40				45				
Gln	His	Ile	Gly	Ala	Glu	Gly	Glu	Leu	Cys	Val	Ser	Val	Gly	Asp	Lys
			50				55			60					
Val	Leu	Arg	Gly	Gln	Pro	Leu	Thr	Arg	Gly	Arg	Gly	Lys	Met	Leu	Pro
			65				70			75			80		
Val	His	Ala	Pro	Thr	Ser	Gly	Thr	Val	Thr	Ala	Ile	Ala	Pro	His	Ser
				85				90			95				
Thr	Ala	His	Pro	Ser	Ala	Leu	Ala	Glu	Leu	Ser	Val	Ile	Ile	Asp	Ala
			100					105			110				
Asp	Gly	Glu	Asp	Cys	Trp	Ile	Pro	Arg	Asp	Gly	Trp	Ala	Asp	Tyr	Arg
			115				120				125				
Thr	Arg	Ser	Arg	Glu	Glu	Leu	Ile	Glu	Arg	Ile	His	Gln	Phe	Gly	Val
			130				135			140					
Ala	Gly	Leu	Gly	Gly	Ala	Gly	Phe	Pro	Thr	Gly	Val	Lys	Leu	Gln	Gly
			145				150			155			160		
Gly	Gly	Asp	Lys	Ile	Glu	Thr	Leu	Ile	Ile	Asn	Ala	Ala	Glu	Cys	Glu
				165				170			175				
Pro	Tyr	Ile	Thr	Ala	Asp	Asp	Arg	Leu	Met	Gln	Asp	Cys	Ala	Ala	Gln
			180				185			190					
Val	Val	Glu	Gly	Ile	Arg	Ile	Leu	Ala	His	Ile	Leu	Gln	Pro	Arg	Glu
			195				200			205					
Ile	Leu	Ile	Gly	Ile	Glu	Asp	Asn	Lys	Pro	Gln	Ala	Ile	Ser	Met	Leu
			210				215			220					
Arg	Ala	Val	Leu	Ala	Asp	Ser	Asn	Asp	Ile	Ser	Leu	Arg	Val	Ile	Pro
			225				230			235			240		
Thr	Lys	Tyr	Pro	Ser	Gly	Gly	Ala	Lys	Gln	Leu	Thr	Tyr	Ile	Leu	Thr
				245				250			255				
Gly	Lys	Gln	Val	Pro	His	Gly	Gly	Arg	Ser	Ser	Asp	Ile	Gly	Val	Leu
			260				265			270					
Met	Gln	Asn	Val	Gly	Thr	Ala	Tyr	Ala	Val	Lys	Arg	Ala	Val	Ile	Asp
			275				280			285					

Gly Glu Pro Ile Thr Glu Arg Val Val Thr Leu Thr Gly Glu Ala Ile
 290 295 300
 Ala Arg Pro Gly Asn Val Trp Ala Arg Leu Gly Thr Pro Val Arg His
 305 310 315 320
 Leu Leu Asn Asp Ala Gly Phe Cys Pro Ser Ala Asp Gln Met Val Ile
 325 330 335
 Met Gly Gly Pro Leu Met Gly Phe Thr Leu Pro Trp Leu Asp Val Pro
 340 345 350
 Val Val Lys Ile Thr Asn Cys Leu Leu Ala Pro Ser Ala Asn Glu Leu
 355 360 365
 Gly Glu Pro Gln Glu Glu Gln Ser Cys Ile Arg Cys Ser Ala Cys Ala
 370 375 380
 Asp Ala Cys Pro Ala Asp Leu Leu Pro Gln Gln Leu Tyr Trp Phe Ser
 385 390 395 400
 Lys Gly Gln Gln His Asp Lys Ala Thr Thr His Asn Ile Ala Asp Cys
 405 410 415
 Ile Glu Cys Gly Ala Cys Ala Trp Val Cys Pro Ser Asn Ile Pro Leu
 420 425 430
 Val Gln Tyr Phe Arg Gln Glu Lys Ala Glu Ile Ala Ala Ile Arg Gln
 435 440 445
 Glu Glu Lys Arg Ala Ala Glu Ala Lys Ala Arg Phe Glu Ala Arg Gln
 450 455 460
 Ala Arg Leu Glu Arg Glu Lys Ala Ala Arg Leu Glu Arg His Lys Ser
 465 470 475 480
 Ala Ala Val Gln Pro Ala Ala Lys Asp Lys Asp Ala Ile Ala Ala Ala
 485 490 495
 Leu Ala Arg Val Lys Glu Lys Gln Ala Gln Ala Thr Gln Pro Ile Val
 500 505 510
 Ile Lys Ala Gly Glu Arg Pro Asp Asn Ser Ala Ile Ile Ala Ala Arg
 515 520 525
 Glu Ala Arg Lys Ala Gln Ala Arg Ala Lys Gln Ala Glu Leu Gln Gln
 530 535 540
 Thr Asn Asp Ala Ala Thr Val Ala Asp Pro Arg Lys Thr Ala Val Glu
 545 550 555 560
 Ala Ala Ile Ala Arg Ala Lys Ala Arg Lys Leu Glu Gln Gln Ala
 565 570 575
 Asn Ala Glu Pro Glu Gln Gln Val Asp Pro Arg Lys Ala Ala Val Glu
 580 585 590
 Ala Ala Ile Ala Arg Ala Lys Ala Arg Lys Leu Glu Gln Gln Ala
 595 600 605
 Asn Ala Glu Pro Glu Glu Gln Val Asp Pro Arg Lys Ala Ala Val Glu
 610 615 620
 Ala Ala Ile Ala Arg Ala Lys Ala Arg Lys Leu Glu Gln Gln Ala
 625 630 635 640
 Asn Ala Glu Pro Glu Gln Gln Val Asp Pro Arg Lys Ala Ala Val Glu
 645 650 655
 Ala Ala Ile Ala Arg Ala Lys Ala Arg Lys Arg Glu Gln Gln Pro Ala
 660 665 670
 Asn Ala Glu Pro Glu Glu Gln Val Asp Pro Arg Lys Ala Ala Val Glu
 675 680 685
 Ala Ala Ile Ala Arg Ala Lys Ala Arg Lys Leu Glu Gln Gln Ala
 690 695 700
 Asn Ala Val Pro Glu Glu Gln Val Asp Pro Arg Lys Ala Ala Val Ala
 705 710 715 720
 Ala Ala Ile Ala Arg Ala Gln Ala Lys Lys Ala Ala Gln Gln Lys Val
 725 730 735
 Val Asn Glu Asp

<210> 293
<211> 352
<212> PRT
<213> E. Coli

<400> 293

Met	Val	Phe	Arg	Ile	Ala	Ser	Ser	Pro	Tyr	Thr	His	Asn	Gln	Arg	Gln
1		5							10					15	
Thr	Ser	Arg	Ile	Met	Leu	Leu	Val	Leu	Leu	Ala	Ala	Val	Pro	Gly	Ile
				20				25						30	
Ala	Ala	Gln	Leu	Trp	Phe	Phe	Gly	Trp	Gly	Thr	Leu	Val	Gln	Ile	Leu
		35				40					45				
Leu	Ala	Ser	Val	Ser	Ala	Leu	Leu	Ala	Glu	Ala	Leu	Val	Leu	Lys	Leu
		50				55					60				
Arg	Lys	Gln	Ser	Val	Ala	Ala	Thr	Leu	Lys	Asp	Asn	Ser	Ala	Leu	Leu
65					70				75					80	
Thr	Gly	Leu	Leu	Leu	Ala	Val	Ser	Ile	Pro	Pro	Leu	Ala	Pro	Trp	Trp
						85		90						95	
Met	Val	Val	Leu	Gly	Thr	Val	Phe	Ala	Val	Ile	Ile	Ala	Lys	Gln	Leu
						100		105					110		
Tyr	Gly	Gly	Leu	Gly	Gln	Asn	Pro	Phe	Asn	Pro	Ala	Met	Ile	Gly	Tyr
		115				120					125				
Val	Val	Leu	Leu	Ile	Ser	Phe	Pro	Val	Gln	Met	Thr	Ser	Trp	Leu	Pro
		130				135				140					
Pro	His	Glu	Ile	Ala	Val	Asn	Ile	Pro	Gly	Phe	Ile	Asp	Ala	Ile	Gln
145					150				155					160	
Val	Ile	Phe	Ser	Gly	His	Thr	Ala	Ser	Gly	Gly	Asp	Met	Asn	Thr	Leu
					165				170					175	
Arg	Leu	Gly	Ile	Asp	Gly	Ile	Ser	Gln	Ala	Thr	Pro	Leu	Asp	Thr	Phe
					180			185					190		
Lys	Thr	Ser	Val	Arg	Ala	Gly	His	Ser	Val	Glu	Gln	Ile	Met	Gln	Tyr
					195			200				205			
Pro	Ile	Tyr	Ser	Gly	Ile	Leu	Ala	Gly	Ala	Gly	Trp	Gln	Trp	Val	Asn
					210			215			220				
Leu	Ala	Trp	Leu	Ala	Gly	Gly	Val	Trp	Leu	Leu	Trp	Gln	Lys	Ala	Ile
225					230				235				240		
Arg	Trp	His	Ile	Pro	Leu	Ser	Phe	Leu	Val	Thr	Leu	Ala	Leu	Cys	Ala
					245			250					255		
Met	Leu	Gly	Trp	Leu	Phe	Ser	Pro	Glu	Thr	Leu	Ala	Ala	Pro	Gln	Ile
					260			265					270		
His	Leu	Leu	Ser	Gly	Ala	Thr	Met	Leu	Gly	Ala	Phe	Phe	Ile	Leu	Thr
					275			280				285			
Asp	Pro	Val	Thr	Ala	Ser	Thr	Thr	Asn	Arg	Gly	Arg	Leu	Ile	Phe	Gly
					290			295			300				
Ala	Leu	Ala	Gly	Leu	Leu	Val	Trp	Leu	Ile	Arg	Ser	Phe	Gly	Gly	Tyr
305						310				315				320	
Pro	Asp	Gly	Val	Ala	Phe	Ala	Val	Leu	Leu	Ala	Asn	Ile	Thr	Val	Pro
					325			330					335		
Leu	Ile	Asp	Tyr	Tyr	Thr	Arg	Pro	Arg	Val	Tyr	Gly	His	Arg	Lys	Gly
					340			345					350		

<210> 294

<211> 206
<212> PRT
<213> E. Coli

<400> 294

Met Leu Lys Thr Ile Arg Lys His Gly Ile Thr Leu Ala Leu Phe Ala
1 5 10 15
Ala Gly Ser Thr Gly Leu Thr Ala Ala Ile Asn Gln Met Thr Lys Thr
20 25 30
Thr Ile Ala Glu Gln Ala Ser Leu Gln Gln Lys Ala Leu Phe Asp Gln
35 40 45
Val Leu Pro Ala Glu Arg Tyr Asn Asn Ala Leu Ala Gln Ser Cys Tyr
50 55 60
Leu Val Thr Ala Pro Glu Leu Gly Lys Gly Glu His Arg Val Tyr Ile
65 70 75 80
Ala Lys Gln Asp Asp Lys Pro Val Ala Ala Val Leu Glu Ala Thr Ala
85 90 95
Pro Asp Gly Tyr Ser Gly Ala Ile Gln Leu Leu Val Gly Ala Asp Phe
100 105 110
Asn Gly Thr Val Leu Gly Thr Arg Val Thr Glu His His Glu Thr Pro
115 120 125
Gly Leu Gly Asp Lys Ile Glu Leu Arg Leu Ser Asp Trp Ile Thr His
130 135 140
Phe Ala Gly Lys Ile Ser Gly Ala Asp Asp Ala His Trp Ala Val
145 150 155 160
Lys Lys Asp Gly Asp Phe Asp Gln Phe Thr Gly Ala Thr Ile Thr
165 170 175
Pro Arg Ala Val Val Asn Ala Val Lys Arg Ala Gly Leu Tyr Ala Gln
180 185 190
Thr Leu Pro Ala Gln Leu Ser Gln Leu Pro Ala Cys Gly Glu
195 200 205

<210> 295
<211> 231
<212> PRT
<213> E. Coli

<400> 295

Met Ser Glu Ile Lys Asp Val Ile Val Gln Gly Leu Trp Lys Asn Asn
1 5 10 15
Ser Ala Leu Val Gln Leu Leu Gly Leu Cys Pro Leu Leu Ala Val Thr
20 25 30
Ser Thr Ala Thr Asn Ala Leu Gly Leu Gly Leu Ala Thr Thr Leu Val
35 40 45
Leu Thr Leu Thr Asn Leu Thr Ile Ser Thr Leu Arg His Trp Thr Pro
50 55 60
Ala Glu Ile Arg Ile Pro Ile Tyr Val Met Ile Ile Ala Ser Val Val
65 70 75 80
Ser Ala Val Gln Met Leu Ile Asn Ala Tyr Ala Phe Gly Leu Tyr Gln
85 90 95
Ser Leu Gly Ile Phe Ile Pro Leu Ile Val Thr Asn Cys Ile Val Val
100 105 110
Gly Arg Ala Glu Ala Phe Ala Ala Lys Lys Gly Pro Ala Leu Ser Ala
115 120 125
Leu Asp Gly Phe Ser Ile Gly Met Gly Ala Thr Cys Ala Met Phe Val
130 135 140

Leu Gly Ser Leu Arg Glu Ile Ile Gly Asn Gly Thr Leu Phe Asp Gly
 145 150 155 160
 Ala Asp Ala Leu Leu Gly Ser Trp Ala Lys Val Leu Arg Val Glu Ile
 165 170 175
 Phe His Thr Asp Ser Pro Phe Leu Leu Ala Met Leu Pro Pro Gly Ala
 180 185 190
 Phe Ile Gly Leu Gly Leu Met Leu Ala Gly Lys Tyr Leu Ile Asp Glu
 195 200 205
 Arg Met Lys Lys Arg Arg Ala Glu Ala Ala Ala Glu Arg Ala Leu Pro
 210 215 220
 Asn Gly Glu Thr Gly Asn Val
 225 230

<210> 296
 <211> 211
 <212> PRT
 <213> E. Coli

<400> 296
 Met Asn Lys Ala Lys Arg Leu Glu Ile Leu Thr Arg Leu Arg Glu Asn
 1 5 10 15
 Asn Pro His Pro Thr Thr Glu Leu Asn Phe Ser Ser Pro Phe Glu Leu
 20 25 30
 Leu Ile Ala Val Leu Leu Ser Ala Gln Ala Thr Asp Val Ser Val Asn
 35 40 45
 Lys Ala Thr Ala Lys Leu Tyr Pro Val Ala Asn Thr Pro Ala Ala Met
 50 55 60
 Leu Glu Leu Gly Val Glu Gly Val Lys Thr Tyr Ile Lys Thr Ile Gly
 65 70 75 80
 Leu Tyr Asn Ser Lys Ala Glu Asn Ile Ile Lys Thr Cys Arg Ile Leu
 85 90 95
 Leu Glu Gln His Asn Gly Glu Val Pro Glu Asp Arg Ala Ala Leu Glu
 100 105 110
 Ala Leu Pro Gly Val Gly Arg Lys Thr Ala Asn Val Val Leu Asn Thr
 115 120 125
 Ala Phe Gly Trp Pro Thr Ile Ala Val Asp Thr His Ile Phe Arg Val
 130 135 140
 Cys Asn Arg Thr Gln Phe Ala Pro Gly Lys Asn Val Glu Gln Val Glu
 145 150 155 160
 Glu Lys Leu Leu Lys Val Val Pro Ala Glu Phe Lys Val Asp Cys His
 165 170 175
 His Trp Leu Ile Leu His Gly Arg Tyr Thr Cys Ile Ala Arg Lys Pro
 180 185 190
 Arg Cys Gly Ser Cys Ile Ile Glu Asp Leu Cys Glu Tyr Lys Glu Lys
 195 200 205
 Val Asp Ile
 210

<210> 297
 <211> 167
 <212> PRT
 <213> E. Coli

<400> 297

Met Lys Arg Leu His Lys Arg Phe Leu Leu Ala Thr Phe Cys Ala Leu

1	5	10	15												
Phe	Thr	Ala	Thr	Leu	Gln	Ala	Ala	Asp	Val	Thr	Ile	Thr	Val	Asn	Gly
				20				25						30	
Arg	Val	Val	Ala	Lys	Pro	Cys	Thr	Ile	Gln	Thr	Lys	Glu	Ala	Asn	Val
				35				40				45			
Asn	Leu	Gly	Asp	Leu	Tyr	Thr	Arg	Asn	Leu	Gln	Gln	Pro	Gly	Ser	Ala
				50				55			60				
Ser	Gly	Trp	His	Asn	Ile	Thr	Leu	Ser	Leu	Thr	Asp	Cys	Pro	Val	Glu
				65				70			75			80	
Thr	Ser	Ala	Val	Thr	Ala	Ile	Val	Thr	Gly	Ser	Thr	Asp	Asn	Thr	Gly
				85				90				95			
Tyr	Tyr	Lys	Asn	Glu	Gly	Thr	Ala	Glu	Asn	Ile	Gln	Ile	Glu	Leu	Arg
				100				105				110			
Asp	Asp	Gln	Asp	Ala	Ala	Leu	Lys	Asn	Gly	Asp	Ser	Lys	Thr	Val	Ile
				115				120				125			
Val	Asp	Glu	Ile	Thr	Arg	Asn	Ala	Gln	Phe	Pro	Leu	Lys	Ala	Arg	Ala
				130				135			140				
Ile	Thr	Val	Asn	Gly	Asn	Ala	Ser	Gln	Gly	Thr	Ile	Glu	Ala	Leu	Ile
				145				150			155			160	
Asn	Val	Ile	Tyr	Thr	Trp	Gln									
				165											

<210> 298
 <211> 176
 <212> PRT
 <213> E. Coli

<400>	298														
Met	Lys	Tyr	Asn	Asn	Ile	Ile	Phe	Leu	Gly	Leu	Cys	Leu	Gly	Leu	Thr
1					5				10					15	
Thr	Tyr	Ser	Ala	Leu	Ser	Ala	Asp	Ser	Val	Ile	Lys	Ile	Ser	Gly	Arg
					20				25				30		
Val	Leu	Asp	Tyr	Gly	Cys	Thr	Val	Ser	Ser	Asp	Ser	Leu	Asn	Phe	Thr
					35				40			45			
Val	Asp	Leu	Gln	Lys	Asn	Ser	Ala	Arg	Gln	Phe	Pro	Thr	Thr	Gly	Ser
					50				55			60			
Thr	Ser	Pro	Ala	Val	Pro	Phe	Gln	Ile	Thr	Leu	Ser	Glu	Cys	Ser	Lys
					65				70			75		80	
Gly	Thr	Thr	Gly	Val	Arg	Val	Ala	Phe	Asn	Gly	Ile	Glu	Asp	Ala	Glu
					85				90			95			
Asn	Asn	Thr	Leu	Leu	Lys	Leu	Asp	Glu	Gly	Ser	Asn	Thr	Ala	Ser	Gly
					100				105			110			
Leu	Gly	Ile	Glu	Ile	Leu	Asp	Ala	Asn	Met	Arg	Pro	Val	Lys	Leu	Asn
					115				120			125			
Asp	Leu	His	Ala	Gly	Met	Gln	Trp	Ile	Pro	Leu	Val	Pro	Glu	Gln	Asn
					130				135			140			
Asn	Ile	Leu	Pro	Tyr	Ser	Ala	Arg	Leu	Lys	Ser	Thr	Gln	Lys	Ser	Val
					145				150			155		160	
Asn	Pro	Gly	Leu	Val	Arg	Ala	Ser	Ala	Thr	Phe	Thr	Leu	Glu	Phe	Gln
					165				170			175			

<210> 299
 <211> 382

<212> PRT

<213> E. Coli

<400> 299

Met Ser Gly Tyr Thr Val Lys Pro Pro Thr Gly Asp Thr Asn Glu Gln
1 5 10 15
Thr Gln Phe Ile Asp Tyr Phe Asn Leu Phe Tyr Ser Lys Arg Gly Gln
20 25 30
Glu Gln Ile Ser Ile Ser Gln Gln Leu Gly Asn Tyr Gly Thr Thr Phe
35 40 45
Phe Ser Ala Ser Arg Gln Ser Tyr Trp Asn Thr Ser Arg Ser Asp Gln
50 55 60
Gln Ile Ser Phe Gly Leu Asn Val Pro Phe Gly Asp Ile Thr Thr Ser
65 70 75 80
Leu Asn Tyr Ser Tyr Ser Asn Asn Ile Trp Gln Asn Asp Arg Asp His
85 90 95
Leu Leu Ala Phe Thr Leu Asn Val Pro Phe Ser His Trp Met Arg Thr
100 105 110
Asp Ser Gln Ser Ala Phe Arg Asn Ser Asn Ala Ser Tyr Ser Met Ser
115 120 125
Asn Asp Leu Lys Gly Gly Met Thr Asn Leu Ser Gly Val Tyr Gly Thr
130 135 140
Leu Leu Pro Asp Asn Asn Leu Asn Tyr Ser Val Gln Val Gly Asn Thr
145 150 155 160
His Gly Gly Asn Thr Ser Ser Gly Thr Ser Gly Tyr Ser Ser Leu Asn
165 170 175
Tyr Arg Gly Ala Tyr Gly Asn Thr Asn Val Gly Tyr Ser Arg Ser Gly
180 185 190
Asp Ser Ser Gln Ile Tyr Tyr Gly Met Ser Gly Gly Ile Ile Ala His
195 200 205
Ala Asp Gly Ile Thr Phe Gly Gln Pro Leu Gly Asp Thr Met Val Leu
210 215 220
Val Lys Ala Pro Gly Ala Asp Asn Val Lys Ile Glu Asn Gln Thr Gly
225 230 235 240
Ile His Thr Asp Trp Arg Gly Tyr Ala Ile Leu Pro Phe Ala Thr Glu
245 250 255
Tyr Arg Glu Asn Arg Val Ala Leu Asn Ala Asn Ser Leu Ala Asp Asn
260 265 270
Val Glu Leu Asp Glu Thr Val Val Thr Val Ile Pro Thr His Gly Ala
275 280 285
Ile Ala Arg Ala Thr Phe Asn Ala Gln Ile Gly Gly Lys Val Leu Met
290 295 300
Thr Leu Lys Tyr Gly Asn Lys Ser Val Pro Phe Gly Ala Ile Val Thr
305 310 315 320
His Gly Glu Asn Lys Asn Gly Ser Ile Val Ala Glu Asn Gly Gln Val
325 330 335
Tyr Leu Thr Gly Leu Pro Gln Ser Gly Gln Leu Gln Val Ser Trp Gly
340 345 350
Lys Asp Lys Asn Ser Asn Cys Ile Val Glu Tyr Lys Leu Pro Glu Val
355 360 365
Ser Pro Gly Thr Leu Leu Asn Gln Gln Thr Ala Ile Cys Arg
370 375 380

<210> 300

<211> 138

<212> PRT

<213> E. Coli

<400> 300

Met	Ile	Ala	Ile	Ala	Asp	Ile	Leu	Gln	Ala	Gly	Glu	Lys	Leu	Thr	Ala
1						5				10					15
Val	Ala	Pro	Phe	Leu	Ala	Gly	Ile	Gln	Asn	Glu	Glu	Gln	Tyr	Thr	Gln
						20			25					30	
Ala	Leu	Glu	Leu	Val	Asp	His	Leu	Leu	Leu	Asn	Asp	Pro	Glu	Asn	Pro
						35			40				45		
Leu	Leu	Asp	Leu	Val	Cys	Ala	Lys	Ile	Thr	Ala	Trp	Glu	Glu	Ser	Ala
						50			55			60			.
Pro	Glu	Phe	Ala	Glu	Phe	Asn	Ala	Met	Ala	Gln	Ala	Met	Pro	Gly	Gly
65						70				75				80	
Ile	Ala	Val	Ile	Arg	Thr	Leu	Met	Asp	Gln	Tyr	Gly	Leu	Thr	Leu	Ser
						85			90				95		
Asp	Leu	Pro	Glu	Ile	Gly	Ser	Lys	Ser	Met	Val	Ser	Arg	Val	Leu	Ser
						100			105			110			
Gly	Lys	Arg	Lys	Leu	Thr	Leu	Glu	His	Ala	Lys	Lys	Leu	Ala	Thr	Arg
						115			120			125			
Phe	Gly	Ile	Ser	Pro	Ala	Leu	Phe	Ile	Asp						
						130			135						

<210> 301

<211> 104

<212> PRT

<213> E. Coli

<400> 301

Met	His	Leu	Ile	Thr	Gln	Lys	Ala	Leu	Lys	Asp	Ala	Ala	Glu	Lys	Tyr
1						5			10					15	
Pro	Gln	His	Lys	Thr	Glu	Leu	Val	Ala	Leu	Gly	Asn	Thr	Ile	Ala	Lys
						20			25				30		
Gly	Tyr	Phe	Lys	Pro	Glu	Ser	Leu	Lys	Ala	Val	Phe	Pro	Ser	Leu	
						35			40			45			
Asp	Asn	Phe	Lys	Tyr	Leu	Asp	Lys	His	Tyr	Val	Phe	Asn	Val	Gly	Gly
						50			55			60			
Asn	Glu	Leu	Arg	Val	Val	Ala	Met	Val	Phe	Phe	Glu	Ser	Gln	Lys	Cys
65						70			75			80			
Tyr	Ile	Arg	Glu	Val	Met	Thr	His	Lys	Glu	Tyr	Asp	Phe	Phe	Thr	Ala
						85			90			95			
Val	His	Arg	Thr	Lys	Gly	Lys	Lys								
						100									

<210> 302

<211> 2383

<212> PRT

<213> E. Coli

<400> 302

Met	Leu	Ser	Val	Phe	Thr	Phe	Phe	Arg	Cys	Ala	Arg	Lys	Gly	Ala	Phe
1						5			10					15	
Met	Leu	Ala	Arg	Ser	Gly	Lys	Val	Ser	Met	Ala	Thr	Lys	Lys	Arg	Ser
						20			25			30			
Gly	Glu	Glu	Ile	Asn	Asp	Arg	Gln	Ile	Leu	Cys	Gly	Met	Gly	Ile	Lys

35	40	45
Leu Arg Arg Leu Thr Ala Gly Ile Cys Leu Ile Thr Gln Leu Ala Phe		
50	55	60
Pro Met Ala Ala Ala Ala Gln Gly Val Val Asn Ala Ala Thr Gln Gln		
65	70	75
80		
Pro Val Pro Ala Gln Ile Ala Ile Ala Asn Ala Asn Thr Val Pro Tyr		
85	90	95
Thr Leu Gly Ala Leu Glu Ser Ala Gln Ser Val Ala Glu Arg Phe Gly		
100	105	110
Ile Ser Val Ala Glu Leu Arg Lys Leu Asn Gln Phe Arg Thr Phe Ala		
115	120	125
Arg Ser Phe Asp Asn Val Arg Gln Gly Asp Glu Leu Asp Val Pro Ala		
130	135	140
Gln Val Ser Glu Lys Lys Leu Thr Pro Pro Gly Asn Ser Ser Asp		
145	150	155
160		
Asn Leu Glu Gln Gln Ile Ala Ser Thr Ser Gln Gln Ile Gly Ser Leu		
165	170	175
Leu Ala Glu Asp Met Asn Ser Glu Gln Ala Ala Asn Met Ala Arg Gly		
180	185	190
Trp Ala Ser Ser Gln Ala Ser Gly Ala Met Thr Asp Trp Leu Ser Arg		
195	200	205
Phe Gly Thr Ala Arg Ile Thr Leu Gly Val Asp Glu Asp Phe Ser Leu		
210	215	220
Lys Asn Ser Gln Phe Asp Phe Leu His Pro Trp Tyr Glu Thr Pro Asp		
225	230	235
240		
Asn Leu Phe Phe Ser Gln His Thr Leu His Arg Thr Asp Glu Arg Thr		
245	250	255
Gln Ile Asn Asn Gly Leu Gly Trp Arg His Phe Thr Pro Thr Trp Met		
260	265	270
Ser Gly Ile Asn Phe Phe Asp His Asp Leu Ser Arg Tyr His Ser		
275	280	285
Arg Ala Gly Ile Gly Ala Glu Tyr Trp Arg Asp Tyr Leu Lys Leu Ser		
290	295	300
Ser Asn Gly Tyr Leu Arg Leu Thr Asn Trp Arg Ser Ala Pro Glu Leu		
305	310	315
320		
Asp Asn Asp Tyr Glu Ala Arg Pro Ala Asn Gly Trp Asp Val Arg Ala		
325	330	335
Glu Ser Trp Leu Pro Ala Trp Pro His Leu Gly Gly Lys Leu Val Tyr		
340	345	350
Glu Gln Tyr Tyr Gly Asp Glu Val Ala Leu Phe Asp Lys Asp Asp Arg		
355	360	365
Gln Ser Asn Pro His Ala Ile Thr Ala Gly Leu Asn Tyr Thr Pro Phe		
370	375	380
Pro Leu Met Thr Phe Ser Ala Glu Gln Arg Gln Gly Lys Gln Gly Glu		
385	390	395
400		
Asn Asp Thr Arg Phe Ala Val Asp Phe Thr Trp Gln Pro Gly Ser Ala		
405	410	415
Met Gln Lys Gln Leu Asp Pro Asn Glu Val Ala Ala Arg Arg Ser Leu		
420	425	430
Ala Gly Ser Arg Tyr Asp Leu Val Asp Arg Asn Asn Asn Ile Val Leu		
435	440	445
Glu Tyr Arg Lys Lys Glu Leu Val Arg Leu Thr Leu Thr Asp Pro Val		
450	455	460
Thr Gly Lys Ser Gly Glu Val Lys Ser Leu Val Ser Ser Leu Gln Thr		
465	470	475
480		
Lys Tyr Ala Leu Lys Gly Tyr Asn Val Glu Ala Thr Ala Leu Glu Ala		
485	490	495

Ala Gly Gly Lys Val Val Thr Thr Gly Lys Asp Ile Leu Val Thr Leu
 500 505 510
 Pro Ala Tyr Arg Phe Thr Ser Thr Pro Glu Thr Asp Asn Thr Trp Pro
 515 520 525
 Ile Glu Val Thr Ala Glu Asp Val Lys Gly Asn Leu Ser Asn Arg Glu
 530 535 540
 Gln Ser Met Val Val Gln Ala Pro Thr Leu Ser Gln Lys Asp Ser
 545 550 555 560
 Ser Val Ser Leu Ser Thr Gln Thr Leu Asn Ala Asp Ser His Ser Thr
 565 570 575
 Ala Thr Leu Thr Phe Ile Ala His Asp Ala Ala Gly Asn Pro Val Val
 580 585 590
 Gly Leu Val Leu Ser Thr Arg His Glu Gly Val Gln Asp Ile Thr Leu
 595 600 605
 Ser Asp Trp Lys Asp Asn Gly Asp Gly Ser Tyr Thr Gln Ile Leu Thr
 610 615 620
 Thr Gly Ala Met Ser Gly Thr Leu Thr Leu Met Pro Gln Leu Asn Gly
 625 630 635 640
 Val Asp Ala Ala Lys Ala Pro Ala Val Val Asn Ile Ile Ser Val Ser
 645 650 655
 Ser Ser Arg Thr His Ser Ser Ile Lys Ile Asp Lys Asp Arg Tyr Leu
 660 665 670
 Ser Gly Asn Pro Ile Glu Val Thr Val Glu Leu Arg Asp Glu Asn Asp
 675 680 685
 Lys Pro Val Lys Glu Gln Lys Gln Gln Leu Asn Asn Ala Val Ser Ile
 690 695 700
 Asp Asn Val Lys Pro Gly Val Thr Thr Asp Trp Lys Glu Thr Ala Asp
 705 710 715 720
 Gly Val Tyr Lys Ala Thr Tyr Thr Ala Tyr Thr Lys Gly Ser Gly Leu
 725 730 735
 Thr Ala Lys Leu Leu Met Gln Asn Trp Asn Glu Asp Leu His Thr Ala
 740 745 750
 Gly Phe Ile Ile Asp Ala Asn Pro Gln Ser Ala Lys Ile Ala Thr Leu
 755 760 765
 Ser Ala Ser Asn Asn Gly Val Leu Ala Asn Glu Asn Ala Ala Asn Thr
 770 775 780
 Val Ser Val Asn Val Ala Asp Glu Gly Ser Asn Pro Ile Asn Asp His
 785 790 795 800
 Thr Val Thr Phe Ala Val Leu Ser Gly Ser Ala Thr Ser Phe Asn Asn
 805 810 815
 Gln Asn Thr Ala Lys Thr Asp Val Asn Gly Leu Ala Thr Phe Asp Leu
 820 825 830
 Lys Ser Ser Lys Gln Glu Asp Asn Thr Val Glu Val Thr Leu Glu Asn
 835 840 845
 Gly Val Lys Gln Thr Leu Ile Val Ser Phe Val Gly Asp Ser Ser Thr
 850 855 860
 Ala Gln Val Asp Leu Gln Lys Ser Lys Asn Glu Val Val Ala Asp Gly
 865 870 875 880
 Asn Asp Ser Val Thr Met Thr Ala Thr Val Arg Asp Ala Lys Gly Asn
 885 890 895
 Leu Leu Asn Asp Val Met Val Thr Phe Asn Val Asn Ser Ala Glu Ala
 900 905 910
 Lys Leu Ser Gln Thr Glu Val Asn Ser His Asp Gly Ile Ala Thr Ala
 915 920 925
 Thr Leu Thr Ser Leu Lys Asn Gly Asp Tyr Arg Val Thr Ala Ser Val
 930 935 940
 Ser Ser Gly Ser Gln Ala Asn Gln Gln Val Asn Phe Ile Gly Asp Gln

945	950	955	960
Ser	Thr Ala Ala Leu Thr Leu Ser Val Pro Ser Gly Asp Ile Thr Val		
965	970	975	
Thr Asn Thr Ala Pro Gln Tyr Met Thr Ala Thr Leu Gln Asp Lys Asn			
980	985	990	
Gly Asn Pro Leu Lys Asp Lys Glu Ile Thr Phe Ser Val Pro Asn Asp			
995	1000	1005	
Val Ala Ser Lys Phe Ser Ile Ser Asn Gly Gly Lys Gly Met Thr Asp			
1010	1015	1020	
Ser Asn Gly Val Ala Ile Ala Ser Leu Thr Gly Thr Leu Ala Gly Thr			
1025	1030	1035	1040
His Met Ile Met Ala Arg Leu Ala Asn Ser Asn Val Ser Asp Ala Gln			
1045	1050	1055	
Pro Met Thr Phe Val Ala Asp Lys Asp Arg Ala Val Val Val Leu Gln			
1060	1065	1070	
Thr Ser Lys Ala Glu Ile Ile Gly Asn Gly Val Asp Glu Thr Thr Leu			
1075	1080	1085	
Thr Ala Thr Val Lys Asp Pro Ser Asn His Pro Val Ala Gly Ile Thr			
1090	1095	1100	
Val Asn Phe Thr Met Pro Gln Asp Val Ala Ala Asn Phe Thr Leu Glu			
1105	1110	1115	1120
Asn Asn Gly Ile Ala Ile Thr Gln Ala Asn Gly Glu Ala His Val Thr			
1125	1130	1135	
Leu Lys Gly Lys Ala Gly Thr His Thr Val Thr Ala Thr Leu Gly			
1140	1145	1150	
Asn Asn Asn Thr Ser Asp Ser Gln Pro Val Thr Phe Val Ala Asp Lys			
1155	1160	1165	
Ala Ser Ala Gln Val Val Leu Gln Ile Ser Lys Asp Glu Ile Thr Gly			
1170	1175	1180	
Asn Gly Val Asp Ser Ala Thr Leu Thr Ala Thr Val Lys Asp Gln Phe			
1185	1190	1195	1200
Asp Asn Glu Val Asn Asn Leu Pro Val Thr Phe Ser Ser Ala Ser Ser			
1205	1210	1215	
Gly Leu Thr Leu Thr Pro Gly Val Ser Asn Thr Asn Glu Ser Gly Ile			
1220	1225	1230	
Ala Gln Ala Thr Leu Ala Gly Val Ala Phe Gly Glu Lys Thr Val Thr			
1235	1240	1245	
Ala Ser Leu Ala Asn Asn Gly Ala Ser Asp Asn Lys Thr Val His Phe			
1250	1255	1260	
Ile Gly Asp Thr Ala Ala Ala Lys Ile Ile Glu Leu Ala Pro Val Pro			
1265	1270	1275	1280
Asp Ser Ile Ile Ala Gly Thr Pro Gln Asn Ser Ser Gly Ser Val Ile			
1285	1290	1295	
Thr Ala Thr Val Val Asp Asn Asn Gly Phe Pro Val Lys Gly Val Thr			
1300	1305	1310	
Val Asn Phe Thr Ser Asn Ala Ala Thr Ala Glu Met Thr Asn Gly Gly			
1315	1320	1325	
Gln Ala Val Thr Asn Glu Gln Gly Lys Ala Thr Val Thr Tyr Thr Asn			
1330	1335	1340	
Thr Arg Ser Ser Ile Glu Ser Gly Ala Arg Pro Asp Thr Val Glu Ala			
1345	1350	1355	1360
Ser Leu Glu Asn Gly Ser Ser Thr Leu Ser Thr Ser Ile Asn Val Asn			
1365	1370	1375	
Ala Asp Ala Ser Thr Ala His Leu Thr Leu Leu Gln Ala Leu Phe Asp			
1380	1385	1390	
Thr Val Ser Ala Gly Glu Thr Thr Ser Leu Tyr Ile Glu Val Lys Asp			
1395	1400	1405	

Asn Tyr Gly Asn Gly Val Pro Gln Gln Glu Val Thr Leu Ser Val Ser
 1410 1415 1420
 Pro Ser Glu Gly Val Thr Pro Ser Asn Asn Ala Ile Tyr Thr Thr Asn
 1425 1430 1435 1440
 His Asp Gly Asn Phe Tyr Ala Ser Phe Thr Ala Thr Lys Ala Gly Val
 1445 1450 1455
 Tyr Gln Leu Thr Ala Thr Leu Glu Asn Gly Asp Ser Met Gln Gln Thr
 1460 1465 1470
 Val Thr Tyr Val Pro Asn Val Ala Asn Ala Glu Ile Thr Leu Ala Ala
 1475 1480 1485
 Ser Lys Asp Pro Val Ile Ala Asp Asn Asn Asp Leu Thr Thr Leu Thr
 1490 1495 1500
 Ala Thr Val Ala Asp Thr Glu Gly Asn Ala Ile Ala Asn Thr Glu Val
 1505 1510 1515 1520
 Thr Phe Thr Leu Pro Glu Asp Val Lys Ala Asn Phe Thr Leu Ser Asp
 1525 1530 1535
 Gly Gly Lys Val Ile Thr Asp Ala Glu Gly Lys Ala Lys Val Thr Leu
 1540 1545 1550
 Lys Gly Thr Lys Ala Gly Ala His Thr Val Thr Ala Ser Met Thr Gly
 1555 1560 1565
 Gly Lys Ser Glu Gln Leu Val Val Asn Phe Ile Ala Asp Thr Leu Thr
 1570 1575 1580
 Ala Gln Val Asn Leu Asn Val Thr Glu Asp Asn Phe Ile Ala Asn Asn
 1585 1590 1595 1600
 Val Gly Met Thr Arg Leu Gln Ala Thr Val Thr Asp Gly Asn Gly Asn
 1605 1610 1615
 Pro Leu Ala Asn Glu Ala Val Thr Phe Thr Leu Pro Ala Asp Val Ser
 1620 1625 1630
 Ala Ser Phe Thr Leu Gly Gln Gly Ser Ala Ile Thr Asp Ile Asn
 1635 1640 1645
 Gly Lys Ala Glu Val Thr Leu Ser Gly Thr Lys Ser Gly Thr Tyr Pro
 1650 1655 1660
 Val Thr Val Ser Val Asn Asn Tyr Gly Val Ser Asp Thr Lys Gln Val
 1665 1670 1675 1680
 Thr Leu Ile Ala Asp Ala Gly Thr Ala Lys Leu Ala Ser Leu Thr Ser
 1685 1690 1695
 Val Tyr Ser Phe Val Val Ser Thr Thr Glu Gly Ala Thr Met Thr Ala
 1700 1705 1710
 Ser Val Thr Asp Ala Asn Gly Asn Pro Val Glu Gly Ile Lys Val Asn
 1715 1720 1725
 Phe Arg Gly Thr Ser Val Thr Leu Ser Ser Thr Ser Val Glu Thr Asp
 1730 1735 1740
 Asp Arg Gly Phe Ala Glu Ile Leu Val Thr Ser Thr Glu Val Gly Leu
 1745 1750 1755 1760
 Lys Thr Val Ser Ala Ser Leu Ala Asp Lys Pro Thr Glu Val Ile Ser
 1765 1770 1775
 Arg Leu Leu Asn Ala Ser Ala Asp Val Asn Ser Ala Thr Ile Thr Ser
 1780 1785 1790
 Leu Glu Ile Pro Glu Gly Gln Val Met Val Ala Gln Asp Val Ala Val
 1795 1800 1805
 Lys Ala His Val Asn Asp Gln Phe Gly Asn Pro Val Ala His Gln Pro
 1810 1815 1820
 Val Thr Phe Ser Ala Glu Pro Ser Ser Gln Met Ile Ile Ser Gln Asn
 1825 1830 1835 1840
 Thr Val Ser Thr Asn Thr Gln Gly Val Ala Glu Val Thr Met Thr Pro
 1845 1850 1855
 Glu Arg Asn Gly Ser Tyr Met Val Lys Ala Ser Leu Pro Asn Gly Ala

1860	1865	1870
Ser Leu Glu Lys Gln Leu Glu Ala Ile Asp Glu Lys	Leu Thr Leu Thr	
1875	1880	1885
Ala Ser Ser Pro Leu Ile Gly Val Tyr Ala Pro Thr	Gly Ala Thr Leu	
1890	1895	1900
Thr Ala Thr Leu Thr Ser Ala Asn Gly Thr Pro	Val Glu Gly Gln Val	
1905	1910	1915
Ile Asn Phe Ser Val Thr Pro Glu Gly Ala Thr Leu	Ser Gly Gly Lys	
1925	1930	1935
Val Arg Thr Asn Ser Ser Gly Gln Ala Pro Val Val	Leu Thr Ser Asn	
1940	1945	1950
Lys Val Gly Thr Tyr Thr Val Thr Ala Ser Phe His	Asn Gly Val Thr	
1955	1960	1965
Ile Gln Thr Gln Thr Thr Val Lys Val Thr Gly Asn	Ser Ser Thr Ala	
1970	1975	1980
His Val Ala Ser Phe Ile Ala Asp Pro Ser Thr	Ile Ala Ala Thr Asn	
1985	1990	1995
Thr Asp Leu Ser Thr Leu Lys Ala Thr Val Glu Asp	Gly Ser Gly Asn	
2005	2010	2015
Leu Ile Glu Gly Leu Thr Val Tyr Phe Ala Leu Lys	Ser Gly Ser Ala	
2020	2025	2030
Thr Leu Thr Ser Leu Thr Ala Val Thr Asp Gln Asn	Gly Ile Ala Thr	
2035	2040	2045
Thr Ser Val Lys Gly Ala Met Thr Gly Ser Val Thr	Val Ser Ala Val	
2050	2055	2060
Thr Thr Ala Gly Gly Met Gln Thr Val Asp Ile Thr	Leu Val Ala Gly	
2065	2070	2075
Pro Ala Asp Thr Ser Gln Ser Val Leu Lys Ser Asn	Arg Ser Ser Leu	
2085	2090	2095
Lys Gly Asp Tyr Thr Asp Ser Ala Glu Leu Arg Leu	Val Leu His Asp	
2100	2105	2110
Ile Ser Gly Asn Pro Ile Lys Val Ser Glu Gly Met	Glu Phe Val Gln	
2115	2120	2125
Ser Gly Thr Asn Val Pro Tyr Ile Lys Ile Ser Ala	Ile Asp Tyr Ser	
2130	2135	2140
Leu Asn Ile Asn Gly Asp Tyr Lys Ala Thr Val Thr	Gly Gly Gly Glu	
2145	2150	2155
Gly Ile Ala Thr Leu Ile Pro Val Leu Asn Gly Val	His Gln Ala Gly	
2165	2170	2175
Leu Ser Thr Thr Ile Gln Phe Thr Arg Ala Glu Asp	Lys Ile Met Ser	
2180	2185	2190
Gly Thr Val Ser Val Asn Gly Thr Asp Leu Pro Thr	Thr Thr Phe Pro	
2195	2200	2205
Ser Gln Gly Phe Thr Gly Ala Tyr Tyr Gln Leu Asn	Asn Asp Asn Phe	
2210	2215	2220
Ala Pro Gly Lys Thr Ala Ala Asp Tyr Glu Phe Ser	Ser Ser Ser Ala Ser	
2225	2230	2235
Trp Val Asp Val Asp Ala Thr Gly Lys Val Thr Phe	Lys Asn Val Gly	
2245	2250	2255
Ser Asn Ser Glu Arg Ile Thr Ala Thr Pro Lys Ser	Gly Gly Pro Ser	
2260	2265	2270
Tyr Val Tyr Glu Ile Arg Val Lys Ser Trp Trp Val	Asn Ala Gly Glu	
2275	2280	2285
Ala Phe Met Ile Tyr Ser Leu Ala Glu Asn Phe Cys	Ser Ser Asn Gly	
2290	2295	2300
Tyr Thr Leu Pro Arg Ala Asn Tyr Leu Asn His Cys	Ser Ser Arg Gly	
2305	2310	2315
		2320

Ile	Gly	Ser	Leu	Tyr	Ser	Glu	Trp	Gly	Asp	Met	Gly	His	Tyr	Thr	Thr
2325								2330							2335
Asp	Ala	Gly	Phe	Gln	Ser	Asn	Met	Tyr	Trp	Ser	Ser	Ser	Pro	Ala	Asn
2340								2345							2350
Ser	Ser	Glu	Gln	Tyr	Val	Val	Ser	Leu	Ala	Thr	Gly	Asp	Gln	Ser	Val
2355							2360							2365	
Phe	Glu	Lys	Leu	Gly	Phe	Ala	Tyr	Ala	Thr	Cys	Tyr	Lys	Asn	Leu	
2370						2375						2380			

<210> 303
<211> 61
<212> PRT
<213> E. Coli

<400> 303

Met	Ser	Lys	Gly	Ala	Leu	Tyr	Glu	Phe	Asn	Asn	Pro	Asp	Gln	Leu	Lys
1				5					10						15
Ile	Pro	Leu	Pro	His	Lys	His	Ile	Ala	Ser	Thr	Phe	Asn	Asp	Ile	Met
				20				25							30
Ser	Lys	Asp	Val	Gly	Tyr	Ala	Tyr	Val	Ser	Leu	Leu	Tyr	Ala	Cys	Pro
				35				40				45			
Leu	Lys	Thr	His	Ser	Leu	Arg	Leu	Asn	Pro	Phe	Ser	Lys			
				50				55				60			

<210> 304
<211> 398
<212> PRT
<213> E. Coli

<400> 304

Met	Gln	Val	Ala	Glu	Gln	Arg	Ile	Gln	Leu	Ala	Glu	Ala	Gln	Ala	Lys
1				5					10						15
Ala	Val	Ala	Thr	Gln	Asp	Gly	Pro	Gln	Ile	Asp	Phe	Ser	Ala	Asp	Met
				20				25							30
Glu	Arg	Gln	Lys	Met	Ser	Ala	Glu	Gly	Leu	Met	Gly	Pro	Phe	Ala	Leu
				35				40			45				
Asn	Asp	Pro	Ala	Ala	Gly	Thr	Thr	Gly	Pro	Trp	Tyr	Thr	Asn	Gly	Thr
				50				55			60				
Phe	Gly	Leu	Thr	Ala	Gly	Trp	His	Leu	Asp	Ile	Trp	Gly	Lys	Asn	Arg
				65				70			75				80
Ala	Glu	Val	Thr	Ala	Arg	Leu	Gly	Thr	Val	Lys	Ala	Arg	Ala	Ala	Glu
					85				90						95
Arg	Glu	Gln	Thr	Arg	Gln	Leu	Leu	Ala	Gly	Ser	Val	Ala	Arg	Leu	Tyr
				100				105							110
Trp	Glu	Trp	Gln	Thr	Gln	Ala	Ala	Leu	Asn	Thr	Val	Leu	Gln	Gln	Ile
				115				120				125			
Glu	Lys	Glu	Gln	Asn	Thr	Ile	Ile	Ala	Thr	Asp	Arg	Gln	Leu	Tyr	Gln
				130				135			140				
Asn	Gly	Ile	Thr	Ser	Ser	Val	Glu	Gly	Val	Glu	Thr	Asp	Ile	Asn	Ala
				145				150			155				160
Ser	Lys	Thr	Arg	Gln	Gln	Leu	Asn	Asp	Val	Ala	Gly	Lys	Met	Lys	Ile
					165				170				175		
Ile	Glu	Ala	Arg	Leu	Ser	Ala	Leu	Thr	Asn	Asn	Gln	Thr	Lys	Ser	Leu
				180				185				190			
Lys	Leu	Lys	Pro	Val	Ala	Leu	Pro	Lys	Val	Ala	Ser	Gln	Leu	Pro	Asp

195	200	205
Glu Leu Gly Tyr Ser Leu Leu Ala Arg Arg Ala Asp Leu Gln Ala Ala		
210	215	220
His Trp Tyr Val Glu Ser Ser Leu Ser Thr Ile Asp Ala Ala Lys Ala		
225	230	235
Ala Phe Tyr Pro Asp Ile Asn Leu Met Ala Phe Leu Gln Gln Asp Ala		240
245	250	255
Leu His Leu Ser Asp Leu Phe Arg His Ser Ala Gln Gln Met Gly Val		
260	265	270
Thr Ala Gly Leu Thr Leu Pro Ile Phe Asp Ser Gly Arg Leu Asn Ala		
275	280	285
Asn Leu Asp Ile Ala Lys Ala Glu Ser Asn Leu Ser Ile Ala Ser Tyr		
290	295	300
Asn Lys Ala Val Val Glu Ala Val Asn Asp Val Ala Arg Ala Ala Ser		
305	310	315
Gln Val Gln Thr Leu Ala Glu Lys Asn Gln His Gln Ala Gln Ile Glu		320
325	330	335
Arg Asp Ala Leu Arg Val Val Gly Leu Ala Gln Ala Arg Phe Asn Ala		
340	345	350
Gly Ile Ile Ala Gly Ser Arg Val Ser Glu Ala Arg Ile Pro Ala Leu		
355	360	365
Arg Glu Arg Ala Asn Gly Leu Leu Leu Gln Gly Gln Trp Leu Asp Ala		
370	375	380
Ser Ile Gln Leu Thr Gly Ala Leu Gly Gly Tyr Lys Arg		
385	390	395

<210> 305

<211> 96

<212> PRT

<213> E. Coli

<400> 305

Met Tyr Cys His Ala Lys Leu Lys Asn Ile Ser Gln His Thr Val Ile		
1	5	10
Ser Ala His Leu Phe Leu Pro Asp Tyr Ser Pro Met Asn Arg Asp Ser		
20	25	30
Phe Tyr Pro Ala Ile Ala Cys Phe Pro Leu Leu Leu Met Leu Ala Gly		
35	40	45
Cys Ala Pro Met His Glu Thr Arg Gln Ala Leu Ser Gln Gln Thr Pro		
50	55	60
Ala Ala Gln Val Asp Thr Ala Leu Pro Thr Ala Leu Lys Met Val Gly		
65	70	75
Gln Thr Ala Asn Gly Gly Trp Ser Ile Thr Ile Ile Asn Ser Leu Pro		80
85	90	95

<210> 306

<211> 315

<212> PRT

<213> E. Coli

<400> 306

Met Arg Val Leu Leu Ala Pro Met Glu Gly Val Leu Asp Ser Leu Val		
1	5	10
Arg Glu Leu Leu Thr Glu Val Asn Asp Tyr Asp Leu Cys Ile Thr Glu		
20	25	30

Phe Val Arg Val Val Asp Gln Leu Leu Pro Val Lys Val Phe His Arg
 35 40 45
 Ile Cys Pro Glu Leu Gln Asn Ala Ser Arg Thr Pro Ser Gly Thr Leu
 50 55 60
 Val Arg Val Gln Leu Leu Gly Gln Phe Pro Gln Trp Leu Ala Glu Asn
 65 70 75 80
 Ala Ala Arg Ala Val Glu Leu Gly Ser Trp Gly Val Asp Leu Asn Cys
 85 90 95
 Gly Cys Pro Ser Lys Thr Val Asn Gly Ser Gly Gly Ala Thr Leu
 100 105 110
 Leu Lys Asp Pro Glu Leu Ile Tyr Gln Gly Ala Lys Ala Met Arg Glu
 115 120 125
 Ala Val Pro Ala His Leu Pro Val Ser Val Lys Val Arg Leu Gly Trp
 130 135 140
 Asp Ser Gly Glu Lys Lys Phe Glu Ile Ala Asp Ala Val Gln Gln Ala
 145 150 155 160
 Gly Ala Thr Glu Leu Val Val His Gly Arg Thr Lys Glu Gln Gly Tyr
 165 170 175
 Arg Ala Glu His Ile Asp Trp Gln Ala Ile Gly Asp Ile Arg Gln Arg
 180 185 190
 Leu Asn Ile Pro Val Ile Ala Asn Gly Glu Ile Trp Asp Trp Gln Ser
 195 200 205
 Ala Gln Gln Cys Met Ala Ile Ser Gly Cys Asp Ala Val Met Ile Gly
 210 215 220
 Arg Gly Ala Leu Asn Ile Pro Asn Leu Ser Arg Val Val Lys Tyr Asn
 225 230 235 240
 Glu Pro Arg Met Pro Trp Pro Glu Val Val Ala Leu Leu Gln Lys Tyr
 245 250 255
 Thr Arg Leu Glu Lys Gln Gly Asp Thr Gly Leu Tyr His Val Ala Arg
 260 265 270
 Ile Lys Gln Trp Leu Ser Tyr Leu Arg Lys Glu Tyr Asp Glu Ala Thr
 275 280 285
 Glu Leu Phe Gln His Val Arg Val Leu Asn Asn Ser Pro Asp Ile Ala
 290 295 300
 Arg Ala Ile Gln Ala Ile Asp Ile Glu Lys Leu
 305 310 315

<210> 307
 <211> 296
 <212> PRT
 <213> E. Coli

<400> 307

Met Thr Ile Ser Thr Thr Ser Thr Pro His Asp Ala Val Phe Lys Ser
 1 5 10 15
 Phe Leu Arg His Pro Asp Thr Ala Arg Asp Phe Ile Asp Ile His Leu
 20 25 30
 Pro Ala Pro Leu Arg Lys Leu Cys Asp Leu Thr Thr Leu Lys Leu Glu
 35 40 45
 Pro Asn Ser Phe Ile Asp Glu Asp Leu Arg Gln Tyr Tyr Ser Asp Leu
 50 55 60
 Leu Trp Ser Val Lys Thr Gln Glu Gly Val Gly Tyr Ile Tyr Val Val
 65 70 75 80
 Ile Glu His Gln Ser Lys Pro Glu Glu Leu Met Ala Phe Arg Met Met
 85 90 95
 Arg Tyr Ser Ile Ala Ala Met Gln Asn His Leu Asp Ala Gly Tyr Lys

	100	105	110												
Glu	Leu	Pro	Leu	Val	Leu	Pro	Met	Leu	Phe	Tyr	His	Gly	Cys	Arg	Ser
	115				120						125				
Pro	Tyr	Pro	Tyr	Ser	Leu	Cys	Trp	Leu	Asp	Glu	Phe	Ala	Glu	Pro	Ala
	130				135						140				
Ile	Ala	Arg	Lys	Ile	Tyr	Ser	Ser	Ala	Phe	Pro	Leu	Val	Asp	Ile	Thr
	145				150					155			160		
Val	Val	Pro	Asp	Asp	Glu	Ile	Met	Gln	His	Arg	Lys	Met	Ala	Leu	Leu
	165							170				175			
Glu	Leu	Ile	Gln	Lys	His	Ile	Arg	Gln	Arg	Asp	Leu	Leu	Gly	Leu	Val
	180							185				190			
Asp	Gln	Ile	Val	Ser	Leu	Leu	Val	Thr	Gly	Asn	Thr	Asn	Asp	Arg	Gln
								195	200			205			
Leu	Lys	Ala	Leu	Phe	Asn	Tyr	Val	Leu	Gln	Thr	Gly	Asp	Ala	Gln	Arg
								210	215			220			
Phe	Arg	Ala	Phe	Ile	Gly	Glu	Ile	Ala	Glu	Arg	Ala	Pro	Gln	Glu	Lys
								225	230			235			240
Glu	Lys	Leu	Met	Thr	Ile	Ala	Asp	Arg	Leu	Arg	Glu	Glu	Gly	Ala	Met
								245		250			255		
Gln	Gly	Lys	His	Glu	Glu	Ala	Leu	Arg	Ile	Ala	Gln	Glu	Met	Leu	Asp
								260		265			270		
Arg	Gly	Leu	Asp	Arg	Glu	Leu	Val	Met	Met	Val	Thr	Arg	Leu	Ser	Pro
								275	280			285			
Asp	Asp	Leu	Ile	Ala	Gln	Ser	His								
					290										295

<210> 308
 <211> 555
 <212> PRT
 <213> E. Coli

	<400> 308														
Met	Ala	Gln	Phe	Val	Tyr	Thr	Met	His	Arg	Val	Gly	Lys	Val	Val	Pro
							1	5	10			15			
Pro	Lys	Arg	His	Ile	Leu	Lys	Asn	Ile	Ser	Leu	Ser	Phe	Phe	Pro	Gly
								20	25			30			
Ala	Lys	Ile	Gly	Val	Leu	Gly	Leu	Asn	Gly	Ala	Gly	Lys	Ser	Thr	Leu
								35	40			45			
Leu	Arg	Ile	Met	Ala	Gly	Ile	Asp	Lys	Asp	Ile	Glu	Gly	Glu	Ala	Arg
							50	55			60				
Pro	Gln	Pro	Asp	Ile	Ile	Gly	Tyr	Leu	Pro	Gln	Glu	Pro	Gln	Leu	
							65	70		75		80			
Asn	Pro	Glu	His	Thr	Val	Arg	Glu	Ser	Ile	Glu	Glu	Ala	Val	Ser	Glu
							85		90			95			
Val	Val	Asn	Ala	Leu	Lys	Arg	Leu	Asp	Glu	Val	Tyr	Ala	Leu	Tyr	Ala
							100		105			110			
Asp	Pro	Asp	Ala	Asp	Phe	Asp	Lys	Leu	Ala	Ala	Glu	Gln	Gly	Arg	Leu
							115		120			125			
Glu	Glu	Ile	Ile	Gln	Ala	His	Asp	Gly	His	Asn	Leu	Asn	Val	Gln	Leu
							130		135			140			
Glu	Arg	Ala	Ala	Asp	Ala	Leu	Arg	Leu	Pro	Asp	Trp	Asp	Ala	Lys	Ile
							145		150		155			160	
Ala	Asn	Leu	Ser	Gly	Gly	Glu	Arg	Arg	Arg	Val	Ala	Leu	Cys	Arg	Leu
							165		170			175			
Leu	Leu	Glu	Lys	Pro	Asp	Met	Leu	Leu	Leu	Asp	Glu	Pro	Thr	Asn	His
						180		185			190				

Leu Asp Ala Glu Ser Val Ala Trp Leu Glu Arg Phe Leu His Asp Phe
 195 200 205
 Glu Gly Thr Val Val Ala Ile Thr His Asp Arg Tyr Phe Leu Asp Asn
 210 215 220
 Val Ala Gly Trp Ile Leu Glu Leu Asp Arg Gly Glu Gly Ile Pro Trp
 225 230 235 240
 Glu Gly Asn Tyr Ser Ser Trp Leu Glu Gln Lys Asp Gln Arg Leu Ala
 245 250 255
 Gln Glu Ala Ser Gln Glu Ala Ala Arg Arg Lys Ser Ile Glu Lys Glu
 260 265 270
 Leu Glu Trp Val Arg Gln Gly Thr Lys Gly Arg Gln Ser Lys Gly Lys
 275 280 285
 Ala Arg Leu Ala Arg Phe Glu Glu Leu Asn Ser Thr Glu Tyr Gln Lys
 290 295 300
 Arg Asn Glu Thr Asn Glu Leu Phe Ile Pro Pro Gly Pro Arg Leu Gly
 305 310 315 320
 Asp Lys Val Leu Glu Val Ser Asn Leu Arg Lys Ser Tyr Gly Asp Arg
 325 330 335
 Leu Leu Ile Asp Asp Leu Ser Phe Ser Ile Pro Lys Gly Ala Ile Val
 340 345 350
 Gly Ile Ile Gly Pro Asn Gly Ala Gly Lys Ser Thr Leu Phe Arg Met
 355 360 365
 Ile Ser Gly Gln Glu Gln Pro Asp Ser Gly Thr Ile Thr Leu Gly Glu
 370 375 380
 Thr Val Lys Leu Ala Ser Val Asp Gln Phe Arg Asp Ser Met Asp Asn
 385 390 395 400
 Ser Lys Thr Val Trp Glu Glu Val Ser Gly Gly Leu Asp Ile Met Lys
 405 410 415
 Ile Gly Asn Thr Glu Met Pro Ser Arg Ala Tyr Val Gly Arg Phe Asn
 420 425 430
 Phe Lys Gly Val Asp Gln Gly Lys Arg Val Gly Glu Leu Ser Gly Gly
 435 440 445
 Glu Arg Gly Arg Leu His Leu Ala Lys Leu Leu Gln Val Gly Gly Asn
 450 455 460
 Met Leu Leu Leu Asp Glu Pro Thr Asn Asp Leu Asp Ile Glu Thr Leu
 465 470 475 480
 Arg Ala Leu Glu Asn Ala Leu Leu Glu Phe Pro Gly Cys Ala Met Val
 485 490 495
 Ile Ser His Asp Arg Trp Phe Leu Asp Arg Ile Ala Thr His Ile Leu
 500 505 510
 Asp Tyr Gln Asp Glu Gly Lys Val Glu Phe Phe Glu Gly Asn Phe Thr
 515 520 525
 Glu Tyr Glu Glu Tyr Lys Lys Arg Thr Leu Gly Ala Asp Ala Leu Glu
 530 535 540
 Pro Lys Arg Ile Lys Tyr Lys Arg Ile Ala Lys
 545 550 555

<210> 309
 <211> 173
 <212> PRT
 <213> E. Coli

<400> 309

Met Ser Lys Pro Lys Tyr Pro Phe Glu Lys Arg Leu Glu Val Val Asn
 1 5 10 15

His Tyr Phe Thr Thr Asp Asp Gly Tyr Arg Ile Ile Ser Ala Arg Phe
 20 25 30
 Gly Val Pro Arg Thr Gln Val Arg Thr Trp Val Ala Leu Tyr Glu Lys
 35 40 45
 His Gly Glu Lys Gly Leu Ile Pro Lys Pro Lys Gly Val Ser Ala Asp
 50 55 60
 Pro Glu Leu Arg Ile Lys Val Val Lys Ala Val Ile Glu Gln His Met
 65 70 75 80
 Ser Leu Asn Gln Ala Ala Ala His Phe Met Leu Ala Gly Ser Gly Ser
 85 90 95
 Val Ala Arg Trp Leu Lys Val Tyr Glu Glu Arg Gly Glu Ala Gly Leu
 100 105 110
 Arg Ala Leu Lys Ile Gly Thr Lys Arg Asn Ile Ala Ile Ser Val Asp
 115 120 125
 Pro Glu Lys Ala Ala Ser Ala Leu Glu Leu Ser Lys Asp Arg Arg Ile
 130 135 140
 Glu Asp Leu Glu Arg Gln Val Arg Phe Leu Glu Thr Arg Leu Met Tyr
 145 150 155 160
 Leu Lys Lys Leu Lys Ala Leu Ala His Pro Thr Lys Lys
 165 170

<210> 310
 <211> 283
 <212> PRT
 <213> E. Coli

<400> 310
 Met Lys Val Leu Asn Glu Leu Arg Gln Phe Tyr Pro Leu Asp Glu Leu
 1 5 10 15
 Leu Arg Ala Ala Glu Ile Pro Arg Ser Thr Phe Tyr Tyr His Leu Lys
 20 25 30
 Ala Leu Ser Lys Pro Asp Lys Tyr Ala Asp Val Lys Lys Arg Ile Ser
 35 40 45
 Glu Ile Tyr His Glu Asn Arg Gly Arg Tyr Gly Tyr Arg Arg Val Thr
 50 55 60
 Leu Ser Leu His Arg Glu Gly Lys Gln Ile Asn His Lys Ala Val Gln
 65 70 75 80
 Arg Leu Met Gly Thr Leu Ser Leu Lys Ala Ala Ile Lys Val Lys Arg
 85 90 95
 Tyr Arg Ser Tyr Arg Gly Glu Val Gly Gln Thr Ala Pro Asn Val Leu
 100 105 110
 Gln Arg Asp Phe Lys Ala Thr Arg Pro Asn Glu Lys Trp Val Thr Asp
 115 120 125
 Val Thr Glu Phe Ala Val Asn Gly Arg Lys Leu Tyr Leu Ser Pro Val
 130 135 140
 Ile Asp Leu Phe Asn Asn Glu Val Ile Ser Tyr Ser Leu Ser Glu Arg
 145 150 155 160
 Pro Val Met Asn Met Val Glu Asn Met Leu Asp Gln Ala Phe Lys Lys
 165 170 175
 Leu Asn Pro His Glu His Pro Val Leu His Ser Asp Gln Gly Trp Gln
 180 185 190
 Tyr Arg Met Arg Arg Tyr Gln Asn Ile Leu Lys Glu His Gly Ile Lys
 195 200 205
 Gln Ser Met Ser Arg Lys Gly Asn Cys Leu Asp Asn Ala Val Val Glu
 210 215 220
 Cys Phe Phe Gly Thr Leu Lys Ser Glu Cys Phe Tyr Leu Asp Glu Phe

225 230 235 240
Ser Asn Ile Ser Glu Leu Lys Asp Ala Val Thr Glu Tyr Ile Glu Tyr
 245 250 255
Tyr Asn Ser Arg Arg Ile Ser Leu Lys Leu Lys Gly Leu Thr Pro Ile
 260 265 270
Glu Tyr Arg Asn Gln Thr Tyr Met Pro Arg Val
 275 280

<210> 311
<211> 38
<212> PRT
<213> E. Coli

<400> 311
Met Lys Val Arg Ala Ser Val Lys Lys Leu Cys Arg Asn Cys Lys Ile
1 5 10 15
Val Lys Arg Asp Gly Val Ile Arg Val Ile Cys Ser Ala Glu Pro Lys
20 25 30
His Lys Gln Arg Gln Gly
35

<210> 312
<211> 443
<212> PRT
<213> E. Coli

<400> 312
Met Ala Lys Gln Pro Gly Leu Asp Phe Gln Ser Ala Lys Gly Gly Leu
1 5 10 15
Gly Glu Leu Lys Arg Arg Leu Leu Phe Val Ile Gly Ala Leu Ile Val
20 25 30
Phe Arg Ile Gly Ser Phe Ile Pro Ile Pro Gly Ile Asp Ala Ala Val
35 40 45
Leu Ala Lys Leu Leu Glu Gln Gln Arg Gly Thr Ile Ile Glu Met Phe
50 55 60
Asn Met Phe Ser Gly Gly Ala Leu Ser Arg Ala Ser Ile Phe Ala Leu
65 70 75 80
Gly Ile Met Pro Tyr Ile Ser Ala Ser Ile Ile Ile Gln Leu Leu Thr
85 90 95
Val Val His Pro Thr Leu Ala Glu Ile Lys Lys Glu Gly Glu Ser Gly
100 105 110
Arg Arg Lys Ile Ser Gln Tyr Thr Arg Tyr Gly Thr Leu Val Leu Ala
115 120 125
Ile Phe Gln Ser Ile Gly Ile Ala Thr Gly Leu Pro Asn Met Pro Gly
130 135 140
Met Gln Gly Leu Val Ile Asn Pro Gly Phe Ala Phe Tyr Phe Thr Ala
145 150 155 160
Val Val Ser Leu Val Thr Gly Thr Met Phe Leu Met Trp Leu Gly Glu
165 170 175
Gln Ile Thr Glu Arg Gly Ile Gly Asn Gly Ile Ser Ile Ile Phe
180 185 190
Ala Gly Ile Val Ala Gly Leu Pro Pro Ala Ile Ala His Thr Ile Glu
195 200 205
Gln Ala Arg Gln Gly Asp Leu His Phe Leu Val Leu Leu Val Ala
210 215 220
Val Leu Val Phe Ala Val Thr Phe Phe Val Val Phe Val Glu Arg Gly

225	230	235	240
Gln Arg Arg Ile Val Val Asn Tyr Ala Lys Arg Gln Gln Gly Arg Arg			
245	250	255	
Val Tyr Ala Ala Gln Ser Thr His Leu Pro Leu Lys Val Asn Met Ala			
260	265	270	
Gly Val Ile Pro Ala Ile Phe Ala Ser Ser Ile Ile Leu Phe Pro Ala			
275	280	285	
Thr Ile Ala Ser Trp Phe Gly Gly Gly Thr Gly Trp Asn Trp Leu Thr			
290	295	300	
Thr Ile Ser Leu Tyr Leu Gln Pro Gly Gln Pro Leu Tyr Val Leu Leu			
305	310	315	320
Tyr Ala Ser Ala Ile Ile Phe Phe Cys Phe Phe Tyr Thr Ala Leu Val			
325	330	335	
Phe Asn Pro Arg Glu Thr Ala Asp Asn Leu Lys Lys Ser Gly Ala Phe			
340	345	350	
Val Pro Gly Ile Arg Pro Gly Glu Gln Thr Ala Lys Tyr Ile Asp Lys			
355	360	365	
Val Met Thr Arg Leu Thr Leu Val Gly Ala Leu Tyr Ile Thr Phe Ile			
370	375	380	
Cys Leu Ile Pro Glu Phe Met Arg Asp Ala Met Lys Val Pro Phe Tyr			
385	390	395	400
Phe Gly Gly Thr Ser Leu Leu Ile Val Val Val Val Ile Met Asp Phe			
405	410	415	
Met Ala Gln Val Gln Thr Leu Met Met Ser Ser Gln Tyr Glu Ser Ala			
420	425	430	
Leu Lys Lys Ala Asn Leu Lys Gly Tyr Gly Arg			
435	440		

<210> 313
 <211> 144
 <212> PRT
 <213> E. Coli

<400> 313

Met Arg Leu Asn Thr Leu Ser Pro Ala Glu Gly Ser Lys Lys Ala Gly			
1	5	10	15
Lys Arg Leu Gly Arg Gly Ile Gly Ser Gly Leu Gly Lys Thr Gly Gly			
20	25	30	
Arg Gly His Lys Gly Gln Lys Ser Arg Ser Gly Gly Val Arg Arg			
35	40	45	
Gly Phe Glu Gly Gly Gln Met Pro Leu Tyr Arg Arg Leu Pro Lys Phe			
50	55	60	
Gly Phe Thr Ser Arg Lys Ala Ala Ile Thr Ala Glu Ile Arg Leu Ser			
65	70	75	80
Asp Leu Ala Lys Val Glu Gly Gly Val Val Asp Leu Asn Thr Leu Lys			
85	90	95	
Ala Ala Asn Ile Ile Gly Ile Gln Ile Glu Phe Ala Lys Val Ile Leu			
100	105	110	
Ala Gly Glu Val Thr Thr Pro Val Thr Val Arg Gly Leu Arg Val Thr			
115	120	125	
Lys Gly Ala Arg Ala Ala Ile Glu Ala Ala Gly Gly Lys Ile Glu Glu			
130	135	140	

<210> 314

<211> 59
<212> PRT
<213> E. Coli

<400> 314

Met Ala Lys Thr Ile Lys Ile Thr Gln Thr Arg Ser Ala Ile Gly Arg
1 5 10 15
Leu Pro Lys His Lys Ala Thr Leu Leu Gly Leu Gly Leu Arg Arg Ile
20 25 30
Gly His Thr Val Glu Arg Glu Asp Thr Pro Ala Ile Arg Gly Met Ile
35 40 45
Asn Ala Val Ser Phe Met Val Lys Val Glu Glu
50 55

<210> 315

<211> 167

<212> PRT

<213> E. Coli

<400> 315

Met Ala His Ile Glu Lys Gln Ala Gly Glu Leu Gln Glu Lys Leu Ile
1 5 10 15
Ala Val Asn Arg Val Ser Lys Thr Val Lys Gly Gly Arg Ile Phe Ser
20 25 30
Phe Thr Ala Leu Thr Val Val Gly Asp Gly Asn Gly Arg Val Gly Phe
35 40 45
Gly Tyr Gly Lys Ala Arg Glu Val Pro Ala Ala Ile Gln Lys Ala Met
50 55 60
Glu Lys Ala Arg Arg Asn Met Ile Asn Val Ala Leu Asn Asn Gly Thr
65 70 75 80
Leu Gln His Pro Val Lys Gly Val His Thr Gly Ser Arg Val Phe Met
85 90 95
Gln Pro Ala Ser Glu Gly Thr Gly Ile Ile Ala Gly Gly Ala Met Arg
100 105 110
Ala Val Leu Glu Val Ala Gly Val His Asn Val Leu Ala Lys Ala Tyr
115 120 125
Gly Ser Thr Asn Pro Ile Asn Val Val Arg Ala Thr Ile Asp Gly Leu
130 135 140
Glu Asn Met Asn Ser Pro Glu Met Val Ala Ala Lys Arg Gly Lys Ser
145 150 155 160
Val Glu Glu Ile Leu Gly Lys
165

<210> 316

<211> 117

<212> PRT

<213> E. Coli

<400> 316

Met Asp Lys Lys Ser Ala Arg Ile Arg Arg Ala Thr Arg Ala Arg Arg
1 5 10 15
Lys Leu Gln Glu Leu Gly Ala Thr Arg Leu Val Val His Arg Thr Pro
20 25 30
Arg His Ile Tyr Ala Gln Val Ile Ala Pro Asn Gly Ser Glu Val Leu

35	40	45
Val Ala Ala Ser Thr Val Glu Lys Ala Ile Ala Glu Gln Leu Lys Tyr		
50	55	60
Thr Gly Asn Lys Asp Ala Ala Ala Val Gly Lys Ala Val Ala Glu		
65	70	75
		80
Arg Ala Leu Glu Lys Gly Ile Lys Asp Val Ser Phe Asp Arg Ser Gly		
85	90	95
Phe Gln Tyr His Gly Arg Val Gln Ala Leu Ala Asp Ala Ala Arg Glu		
100	105	110
Ala Gly Leu Gln Phe		
115		

<210> 317
<211> 177
<212> PRT
<213> E. Coli

<400> 317		
Met Ser Arg Val Ala Lys Ala Pro Val Val Val Pro Ala Gly Val Asp		
1	5	10
		15
Val Lys Ile Asn Gly Gln Val Ile Thr Ile Lys Gly Lys Asn Gly Glu		
20	25	30
Leu Thr Arg Thr Leu Asn Asp Ala Val Glu Val Lys His Ala Asp Asn		
35	40	45
Thr Leu Thr Phe Gly Pro Arg Asp Gly Tyr Ala Asp Gly Trp Ala Gln		
50	55	60
Ala Gly Thr Ala Arg Ala Leu Leu Asn Ser Met Val Ile Gly Val Thr		
65	70	75
		80
Glu Gly Phe Thr Lys Lys Leu Gln Leu Val Gly Val Gly Tyr Arg Ala		
85	90	95
Ala Val Lys Gly Asn Val Ile Asn Leu Ser Leu Gly Phe Ser His Pro		
100	105	110
Val Asp His Gln Leu Pro Ala Gly Ile Thr Ala Glu Cys Pro Thr Gln		
115	120	125
Thr Glu Ile Val Leu Lys Gly Ala Asp Lys Gln Val Ile Gly Gln Val		
130	135	140
Ala Ala Asp Leu Arg Ala Tyr Arg Arg Pro Glu Pro Tyr Lys Gly Lys		
145	150	155
		160
Gly Val Arg Tyr Ala Asp Glu Val Val Arg Thr Lys Glu Ala Lys Lys		
165	170	175
Lys		

<210> 318
<211> 130
<212> PRT
<213> E. Coli

<400> 318		
Met Ser Met Gln Asp Pro Ile Ala Asp Met Leu Thr Arg Ile Arg Asn		
1	5	10
		15
Gly Gln Ala Ala Asn Lys Ala Ala Val Thr Met Pro Ser Ser Lys Leu		
20	25	30
Lys Val Ala Ile Ala Asn Val Leu Lys Glu Glu Gly Phe Ile Glu Asp		
35	40	45

Phe	Lys	Val	Glu	Gly	Asp	Thr	Lys	Pro	Glu	Leu	Glu	Leu	Thr	Leu	Lys
50							55				60				
Tyr	Phe	Gln	Gly	Lys	Ala	Val	Val	Glu	Ser	Ile	Gln	Arg	Val	Ser	Arg
65						70				75			80		
Pro	Gly	Leu	Arg	Ile	Tyr	Lys	Arg	Lys	Asp	Glu	Leu	Pro	Lys	Val	Met
						85			90				95		
Ala	Gly	Leu	Gly	Ile	Ala	Val	Val	Ser	Thr	Ser	Lys	Gly	Val	Met	Thr
						100			105				110		
Asp	Arg	Ala	Ala	Arg	Gln	Ala	Gly	Leu	Gly	Gly	Glu	Ile	Ile	Cys	Tyr
						115			120				125		
Val	Ala														
															130

<210> 319
<211> 101
<212> PRT
<213> E. Coli

<400> 319

Met	Ala	Lys	Gln	Ser	Met	'Lys	Ala	Arg	Glu	Val	Lys	Arg	Val	Ala	Leu
1					5				10				15		
Ala	Asp	Lys	Tyr	Phe	Ala	Lys	Arg	Ala	Glu	Leu	Lys	Ala	Ile	Ile	Ser
						20			25				30		
Asp	Val	Asn	Ala	Ser	Asp	Glu	Asp	Arg	Trp	Asn	Ala	Val	Leu	Lys	Leu
						35			40				45		
Gln	Thr	Leu	Pro	Arg	Asp	Ser	Ser	Pro	Ser	Arg	Gln	Arg	Asn	Arg	Cys
						50			55				60		
Arg	Gln	Thr	Gly	Arg	Pro	His	Gly	Phe	Leu	Arg	Lys	Phe	Gly	Leu	Ser
						65			70				75		80
Arg	Ile	Lys	Val	Arg	Glu	Ala	Ala	Met	Arg	Gly	Glu	Ile	Pro	Gly	Leu
						85			90						95
Lys	Lys	Ala	Ser	Trp											
					100										

<210> 320
<211> 179
<212> PRT
<213> E. Coli

<400> 320

Met	Ala	Lys	Leu	His	Asp	Tyr	Tyr	Lys	Asp	Glu	Val	Val	Lys	Lys	Leu
1						5				10				15	
Met	Thr	Glu	Phe	Asn	Tyr	Asn	Ser	Val	Met	Gln	Val	Pro	Arg	Val	Glu
						20			25				30		
Lys	Ile	Thr	Leu	Asn	Met	Gly	Val	Gly	Glu	Ala	Ile	Ala	Asp	Lys	Lys
						35			40				45		
Leu	Leu	Asp	Asn	Ala	Ala	Asp	Leu	Ala	Ala	Ile	Ser	Gly	Gln	Lys	
						50			55				60		
Pro	Leu	Ile	Thr	Lys	Ala	Arg	Lys	Ser	Val	Ala	Gly	Phe	Lys	Ile	Arg
						65			70				75		80
Gln	Gly	Tyr	Pro	Ile	Gly	Cys	Lys	Val	Thr	Leu	Arg	Gly	Glu	Arg	Met
						85			90				95		
Trp	Glu	Phe	Phe	Glu	Arg	Leu	Ile	Thr	Ile	Ala	Val	Pro	Arg	Ile	Arg
						100			105				110		

Asp Phe Arg Gly Leu Ser Ala Lys Ser Phe Asp Gly Arg Gly Asn Tyr
 115 120 125
 Ser Met Gly Val Arg Glu Gln Ile Ile Phe Pro Glu Ile Asp Tyr Asp
 130 135 140
 Lys Val Asp Arg Val Arg Gly Leu Asp Ile Thr Ile Thr Thr Ala
 145 150 155 160
 Lys Ser Asp Glu Glu Gly Arg Ala Leu Leu Ala Ala Phe Asp Phe Pro
 165 170 175
 Phe Arg Lys

<210> 321Z
 <211> 104
 <212> PRT
 <213> E. Coli

<400> 321
 Met Ala Ala Lys Ile Arg Arg Asp Asp Glu Val Ile Val Leu Thr Gly
 1 5 10 15
 Lys Asp Lys Gly Lys Arg Gly Lys Val Lys Asn Val Leu Ser Ser Gly
 20 25 30
 Lys Val Ile Val Glu Gly Ile Asn Leu Val Lys Lys His Gln Lys Pro
 35 40 45
 Val Pro Ala Leu Asn Gln Pro Gly Gly Ile Val Glu Lys Glu Ala Ala
 50 55 60
 Ile Gln Val Ser Asn Val Ala Ile Phe Asn Ala Ala Thr Gly Lys Ala
 65 70 75 80
 Asp Arg Val Gly Phe Arg Phe Glu Asp Gly Lys Lys Val Arg Phe Phe
 85 90 95
 Lys Ser Asn Ser Glu Thr Ile Lys
 100

<210> 322
 <211> 123
 <212> PRT
 <213> E. Coli

<400> 322
 Met Ile Gln Glu Gln Thr Met Leu Asn Val Ala Asp Asn Ser Gly Ala
 1 5 10 15
 Arg Arg Val Met Cys Ile Lys Val Leu Gly Gly Ser His Arg Arg Tyr
 20 25 30
 Ala Gly Val Gly Asp Ile Ile Lys Ile Thr Ile Lys Glu Ala Ile Pro
 35 40 45
 Arg Gly Lys Val Lys Lys Gly Asp Val Leu Lys Ala Val Val Val Arg
 50 55 60
 Thr Lys Lys Gly Val Arg Arg Pro Asp Gly Ser Val Ile Arg Phe Asp
 65 70 75 80
 Gly Asn Ala Cys Val Leu Leu Asn Asn Asn Ser Glu Gln Pro Ile Gly
 85 90 95
 Thr Arg Ile Phe Gly Pro Val Thr Arg Glu Leu Arg Ser Glu Lys Phe
 100 105 110
 Met Lys Ile Ile Ser Leu Ala Pro Glu Val Leu
 115 120

<210> 323
<211> 188
<212> PRT
<213> E. Coli

<400> 323

Met Phe Lys Gly Gln Lys Thr Leu Ala Ala Leu Ala Val Ser Leu Leu
1 5 10 15
Phe Thr Ala Pro Val Tyr Ala Ala Asp Glu Gly Ser Gly Glu Ile His
20 25 30
Phe Lys Gly Glu Val Ile Glu Ala Pro Cys Glu Ile His Pro Glu Asp
35 40 45
Ile Asp Lys Asn Ile Asp Leu Gly Gln Val Thr Thr His Ile Asn
50 55 60
Arg Glu His His Ser Asn Lys Val Ala Val Asp Ile Arg Leu Ile Asn
65 70 75 80
Cys Asp Leu Pro Ala Ser Asp Asn Gly Ser Gly Met Pro Val Ser Lys
85 90 95
Val Gly Val Thr Phe Asp Ser Thr Ala Lys Thr Gly Ala Thr Pro
100 105 110
Leu Leu Ser Asn Thr Ser Ala Gly Glu Ala Thr Gly Val Gly Val Arg
115 120 125
Leu Met Asp Lys Asn Asp Gly Asn Ile Val Leu Gly Ser Ala Ala Pro
130 135 140
Asp Leu Asp Leu Asp Ala Ser Ser Ser Glu Gln Thr Leu Asn Phe Phe
145 150 155 160
Ala Trp Met Glu Gln Ile Asp Asn Ala Val Asp Val Thr Ala Gly Glu
165 170 175
Val Thr Ala Asn Ala Thr Tyr Val Leu Asp Tyr Lys
180 185

<210> 324
<211> 427
<212> PRT
<213> E. Coli

<400> 324

Met Ala Asp Thr Lys Ala Lys Leu Thr Leu Asn Gly Asp Thr Ala Val
1 5 10 15
Glu Leu Asp Val Leu Lys Gly Thr Leu Gly Gln Asp Val Ile Asp Ile
20 25 30
Arg Thr Leu Gly Ser Lys Gly Val Phe Thr Phe Asp Pro Gly Phe Thr
35 40 45
Ser Thr Ala Ser Cys Glu Ser Lys Ile Thr Phe Ile Asp Gly Asp Glu
50 55 60
Gly Ile Leu Leu His Arg Gly Phe Pro Ile Asp Gln Leu Ala Thr Asp
65 70 75 80
Ser Asn Tyr Leu Glu Val Cys Tyr Ile Leu Leu Asn Gly Glu Lys Pro
85 90 95
Thr Gln Glu Gln Tyr Asp Glu Phe Lys Thr Thr Val Thr Arg His Thr
100 105 110
Met Ile His Glu Gln Ile Thr Arg Leu Phe His Ala Phe Arg Arg Asp
115 120 125
Ser His Pro Met Ala Val Met Cys Gly Ile Thr Gly Ala Leu Ala Ala
130 135 140

Phe Tyr His Asp Ser Leu Asp Val Asn Asn Pro Arg His Arg Glu Ile
 145 150 155 160
 Ala Ala Phe Arg Leu Leu Ser Lys Met Pro Thr Met Ala Ala Met Cys
 165 170 175
 Tyr Lys Tyr Ser Ile Gly Gln Pro Phe Val Tyr Pro Arg Asn Asp Leu
 180 185 190
 Ser Tyr Ala Gly Asn Phe Leu Asn Met Met Phe Ser Thr Pro Cys Glu
 195 200 205
 Pro Tyr Glu Val Asn Pro Ile Leu Glu Arg Ala Met Asp Arg Ile Leu
 210 215 220
 Ile Leu His Ala Asp His Glu Gln Asn Ala Ser Thr Ser Thr Val Arg
 225 230 235 240
 Thr Ala Gly Ser Ser Gly Ala Asn Pro Phe Ala Cys Ile Ala Ala Gly
 245 250 255
 Ile Ala Ser Leu Trp Gly Pro Ala His Gly Gly Ala Asn Glu Ala Ala
 260 265 270
 Leu Lys Met Leu Glu Glu Ile Ser Ser Val Lys His Ile Pro Glu Phe
 275 280 285
 Val Arg Arg Ala Lys Asp Lys Asn Asp Ser Phe Arg Leu Met Gly Phe
 290 295 300
 Gly His Arg Val Tyr Lys Asn Tyr Asp Pro Arg Ala Thr Val Met Arg
 305 310 315 320
 Glu Thr Cys His Glu Val Leu Lys Glu Leu Gly Thr Lys Asp Asp Leu
 325 330 335
 Leu Glu Val Ala Met Glu Leu Glu Asn Ile Ala Leu Asn Asp Pro Tyr
 340 345 350
 Phe Ile Glu Lys Leu Tyr Pro Asn Val Asp Phe Tyr Ser Gly Ile
 355 360 365
 Ile Leu Lys Ala Met Gly Ile Pro Ser Ser Met Phe Thr Val Ile Phe
 370 375 380
 Ala Met Ala Arg Thr Val Gly Trp Ile Ala His Trp Ser Glu Met His
 385 390 395 400
 Ser Asp Gly Met Lys Ile Ala Arg Pro Arg Gln Leu Tyr Thr Gly Tyr
 405 410 415
 Glu Lys Arg Asp Phe Lys Ser Asp Ile Lys Arg
 420 425

<210> 325
 <211> 477
 <212> PRT
 <213> E. Coli

<400> 325
 Met Lys Val Thr Leu Pro Glu Phe Glu Arg Ala Gly Val Met Val Val
 1 5 10 15
 Gly Asp Val Met Leu Asp Arg Tyr Trp Tyr Gly Pro Thr Ser Arg Ile
 20 25 30
 Ser Pro Glu Ala Pro Val Pro Val Val Lys Val Asn Thr Ile Glu Glu
 35 40 45
 Arg Pro Gly Gly Ala Ala Asn Val Ala Met Asn Ile Ala Ser Leu Gly
 50 55 60
 Ala Asn Ala Arg Leu Val Gly Leu Thr Gly Ile Asp Asp Ala Ala Arg
 65 70 75 80
 Ala Leu Ser Lys Ser Leu Ala Asp Val Asn Val Lys Cys Asp Phe Val
 85 90 95
 Ser Val Pro Thr His Pro Thr Ile Thr Lys Leu Arg Val Leu Ser Arg

	100	105	110												
Asn	Gln	Gln	Leu	Ile	Arg	Leu	Asp	Phe	Glu	Glu	Gly	Phe	Glu	Gly	Val
			115			120						125			
Asp	Pro	Gln	Pro	Leu	His	Glu	Arg	Ile	Asn	Gln	Ala	Leu	Ser	Ser	Ile
			130			135					140				
Gly	Ala	Leu	Val	Leu	Ser	Asp	Tyr	Ala	Lys	Gly	Ala	Leu	Ala	Ser	Val
			145			150				155			160		
Gln	Gln	Met	Ile	Gln	Leu	Ala	Arg	Lys	Ala	Gly	Val	Pro	Val	Leu	Ile
			165			170				175					
Asp	Pro	Lys	Gly	Thr	Asp	Phe	Glu	Arg	Tyr	Arg	Gly	Ala	Thr	Leu	Leu
			180			185					190				
Thr	Pro	Asn	Leu	Ser	Glu	Phe	Glu	Ala	Val	Val	Gly	Lys	Cys	Lys	Thr
			195			200				205					
Glu	Glu	Glu	Ile	Val	Glu	Arg	Gly	Met	Lys	Leu	Ile	Ala	Asp	Tyr	Glu
			210			215				220					
Leu	Ser	Ala	Leu	Leu	Val	Thr	Arg	Ser	Glu	Gln	Gly	Met	Ser	Leu	Leu
			225			230				235			240		
Gln	Pro	Gly	Lys	Ala	Pro	Leu	His	Met	Pro	Thr	Gln	Ala	Gln	Glu	Val
			245			250				255					
Tyr	Asp	Val	Thr	Gly	Ala	Gly	Asp	Thr	Val	Ile	Gly	Val	Leu	Ala	Ala
			260			265				270					
Thr	Leu	Ala	Ala	Gly	Asn	Ser	Leu	Glu	Glu	Ala	Cys	Phe	Phe	Ala	Asn
			275			280				285					
Ala	Ala	Ala	Gly	Val	Val	Val	Gly	Lys	Leu	Gly	Thr	Ser	Thr	Val	Ser
			290			295				300					
Pro	Ile	Glu	Leu	Glu	Asn	Ala	Val	Arg	Gly	Arg	Ala	Asp	Thr	Gly	Phe
			305			310				315			320		
Gly	Val	Met	Thr	Glu	Glu	Glu	Leu	Lys	Leu	Ala	Val	Ala	Ala	Arg	
			325			330				335					
Lys	Arg	Gly	Gly	Lys	Val	Val	Met	Thr	Asn	Gly	Val	Phe	Asp	Ile	Leu
			340			345				350					
His	Ala	Gly	His	Val	Ser	Tyr	Leu	Ala	Asn	Ala	Arg	Lys	Leu	Gly	Asp
			355			360				365					
Arg	Leu	Ile	Val	Ala	Val	Asn	Ser	Asp	Ala	Ser	Thr	Lys	Arg	Leu	Lys
			370			375				380					
Gly	Asp	Ser	Arg	Pro	Val	Asn	Pro	Leu	Glu	Gln	Arg	Met	Ile	Val	Leu
			385			390				395			400		
Gly	Ala	Leu	Glu	Ala	Val	Asp	Trp	Val	Val	Ser	Phe	Glu	Asp	Thr	
			405			410				415					
Pro	Gln	Arg	Leu	Ile	Ala	Gly	Ile	Leu	Pro	Asp	Leu	Leu	Val	Lys	Gly
			420			425				430					
Gly	Asp	Tyr	Lys	Pro	Glu	Glu	Ile	Ala	Gly	Ser	Lys	Glu	Val	Trp	Ala
			435			440				445					
Asn	Gly	Gly	Glu	Val	Leu	Val	Leu	Asn	Phe	Glu	Asp	Gly	Cys	Ser	Thr
			450			455				460					
Thr	Asn	Ile	Ile	Lys	Lys	Ile	Gln	Gln	Asp	Lys	Lys	Gly			
						465				475					

<210> 326

<211> 946

<212> PRT

<213> E. Coli

<400> 326

Met Lys Pro Leu Ser Ser Pro Leu Gln Gln Tyr Trp Gln Thr Val Val
 1 5 10 15

Glu Arg Leu Pro Glu Pro Leu Ala Glu Glu Ser Leu Ser Ala Gln Ala
 20 25 30
 Lys Ser Val Leu Thr Phe Ser Asp Phe Val Gln Asp Ser Val Ile Ala
 35 40 45
 His Pro Glu Trp Leu Thr Glu Leu Glu Ser Gln Pro Pro Gln Ala Asp
 50 55 60
 Glu Trp Gln His Tyr Ala Ala Trp Leu Gln Glu Ala Leu Cys Asn Val
 65 70 75 80
 Ser Asp Glu Ala Gly Leu Met Arg Glu Leu Arg Leu Phe Arg Arg Arg
 85 90 95
 Ile Met Val Arg Ile Ala Trp Ala Gln Thr Leu Ala Leu Val Thr Glu
 100 105 110
 Glu Ser Ile Leu Gln Gln Leu Ser Tyr Leu Ala Glu Thr Leu Ile Val
 115 120 125
 Ala Ala Arg Asp Trp Leu Tyr Asp Ala Cys Cys Arg Glu Trp Gly Thr
 130 135 140
 Pro Cys Asn Ala Gln Gly Glu Ala Gln Pro Leu Leu Ile Leu Gly Met
 145 150 155 160
 Gly Lys Leu Gly Gly Glu Leu Asn Phe Ser Ser Asp Ile Asp Leu
 165 170 175
 Ile Phe Ala Trp Pro Glu His Gly Cys Thr Gln Gly Gly Arg Arg Glu
 180 185 190
 Leu Asp Asn Ala Gln Phe Phe Thr Arg Met Gly Gln Arg Leu Ile Lys
 195 200 205
 Val Leu Asp Gln Pro Thr Gln Asp Gly Phe Val Tyr Arg Val Asp Met
 210 215 220
 Arg Leu Arg Pro Phe Gly Glu Ser Gly Pro Leu Val Leu Ser Phe Ala
 225 230 235 240
 Ala Leu Glu Asp Tyr Tyr Gln Glu Gln Gly Arg Asp Trp Glu Arg Tyr
 245 250 255
 Ala Met Val Lys Ala Arg Ile Met Gly Asp Ser Glu Gly Val Tyr Ala
 260 265 270
 Asn Glu Leu Arg Ala Met Leu Arg Pro Phe Val Phe Arg Arg Tyr Ile
 275 280 285
 Asp Phe Ser Val Ile Gln Ser Leu Arg Asn Met Lys Gly Met Ile Ala
 290 295 300
 Arg Glu Val Arg Arg Arg Gly Leu Thr Asp Asn Ile Lys Leu Gly Ala
 305 310 315 320
 Gly Gly Ile Arg Glu Ile Glu Phe Ile Val Gln Val Phe Gln Leu Ile
 325 330 335
 Arg Gly Gly Arg Glu Pro Ser Leu Gln Ser Arg Ser Leu Leu Pro Thr
 340 345 350
 Leu Ser Ala Ile Ala Glu Leu His Leu Leu Ser Glu Asn Asp Ala Glu
 355 360 365
 Gln Leu Arg Val Ala Tyr Leu Phe Leu Arg Arg Leu Glu Asn Leu Leu
 370 375 380
 Gln Ser Ile Asn Asp Glu Gln Thr Gln Thr Leu Pro Ser Asp Glu Leu
 385 390 395 400
 Asn Arg Ala Arg Leu Ala Trp Ala Met Asp Phe Ala Asp Trp Pro Gln
 405 410 415
 Leu Thr Gly Ala Leu Thr Ala His Met Thr Asn Val Arg Arg Val Phe
 420 425 430
 Asn Glu Leu Ile Gly Asp Asp Glu Ser Glu Thr Gln Glu Glu Ser Leu
 435 440 445
 Ser Glu Gln Trp Arg Glu Leu Trp Gln Asp Ala Leu Gln Glu Asp Asp
 450 455 460
 Thr Thr Pro Val Leu Ala His Leu Ser Glu Asp Asp Arg Lys Gln Val

465	470	475	480
Leu Thr Leu Ile Ala Asp Phe Arg Lys Glu	Leu Asp Lys Arg Thr Ile		
485	490	495	
Gly Pro Arg Gly Arg Gln Val Leu Asp His	Leu Met Pro His Leu Leu		
500	505	510	
Ser Asp Val Cys Ala Arg Glu Asp Ala Ala Val	Thr Leu Ser Arg Ile		
515	520	525	
Thr Ala Leu Leu Val Gly Ile Val Thr Arg Thr	Thr Tyr Leu Glu Leu		
530	535	540	
Leu Ser Glu Phe Pro Ala Ala Leu Lys His	Leu Ile Ser Leu Cys Ala		
545	550	555	560
Ala Ser Pro Met Ile Ala Ser Gln Leu Ala Arg	Tyr Pro Leu Leu Leu		
565	570	575	
Asp Glu Leu Leu Asp Pro Asn Thr Leu Tyr Gln	Pro Thr Ala Thr Asp		
580	585	590	
Ala Tyr Arg Asp Glu Leu Arg Gln Tyr Leu Leu	Arg Val Pro Glu Asp		
595	600	605	
Asp Glu Glu Gln Gln Leu Glu Ala Leu Arg Gln	Phe Lys Gln Ala Gln		
610	615	620	
Leu Leu Arg Ile Ala Ala Ala Asp Ile Ala Gly	Thr Leu Pro Val Met		
625	630	635	640
Lys Val Ser Asp His Leu Thr Trp Leu Ala Glu	Ala Met Ile Asp Ala		
645	650	655	
Val Val Gln Gln Ala Trp Val Gln Met Val Ala	Arg Tyr Gly Lys Pro		
660	665	670	
Asn His Leu Asn Glu Arg Glu Gly Arg Gly	Phe Ala Val Val Gly Tyr		
675	680	685	
Gly Lys Leu Gly Gly Trp Glu Leu Gly Tyr Ser	Ser Asp Leu Asp Leu		
690	695	700	
Ile Phe Leu His Asp Cys Pro Met Asp Ala Met	Thr Asp Gly Glu Arg		
705	710	715	720
Glu Ile Asp Gly Arg Gln Phe Tyr Leu Arg Leu	Ala Gln Arg Ile Met		
725	730	735	
His Leu Phe Ser Thr Arg Thr Ser Ser Gly Ile	Leu Tyr Glu Val Asp		
740	745	750	
Ala Arg Leu Arg Pro Ser Gly Ala Ala Gly Met	Leu Val Thr Ser Ala		
755	760	765	
Glu Ala Phe Ala Asp Tyr Gln Lys Asn Glu	Ala Trp Thr Trp Glu His		
770	775	780	
Gln Ala Leu Val Arg Ala Arg Val Val Tyr	Gly Asp Pro Gln Leu Thr		
785	790	795	800
Ala His Phe Asp Ala Val Arg Arg Glu Ile Met	Thr Leu Pro Arg Glu		
805	810	815	
Gly Lys Thr Leu Gln Thr Glu Val Arg Glu Met	Arg Glu Lys Met Arg		
820	825	830	
Ala His Leu Gly Asn Lys His Arg Asp Arg Phe	Asp Ile Lys Ala Asp		
835	840	845	
Glu Gly Gly Ile Thr Asp Ile Glu Phe Ile Thr	Gln Tyr Leu Val Leu		
850	855	860	
Arg Tyr Ala His Glu Lys Pro Lys Leu Thr Arg	Trp Ser Asp Asn Val		
865	870	875	880
Arg Ile Leu Glu Leu Leu Ala Gln Asn Asp Ile	Met Glu Glu Gln Glu		
885	890	895	
Ala Met Ala Leu Thr Arg Ala Tyr Thr Leu Arg	Asp Glu Leu His		
900	905	910	
His Leu Ala Leu Gln Glu Leu Pro Gly His Val	Ser Glu Asp Cys Phe		
915	920	925	

Thr Ala Glu Arg Glu Leu Val Arg Ala Ser Trp Gln Lys Trp Leu Val		
930	935	940
Glu Glu		
945		

<210> 327
<211> 433
<212> PRT
<213> E. Coli

<400> 327			
Met Ala Gln Glu Ile Glu Leu Lys Phe Ile Val Asn His Ser Ala Val			
1	5	10	15
Glu Ala Leu Arg Asp His Leu Asn Thr Leu Gly Gly Glu His His Asp			
20	25	30	
Pro Val Gln Leu Leu Asn Ile Tyr Tyr Glu Thr Pro Asp Asn Trp Leu			
35	40	45	
Arg Gly His Asp Met Gly Leu Arg Ile Arg Gly Glu Asn Gly Arg Tyr			
50	55	60	
Glu Met Thr Met Lys Val Ala Gly Arg Val Thr Gly Gly Leu His Gln			
65	70	75	80
Arg Pro Glu Tyr Asn Val Ala Leu Ser Glu Pro Thr Leu Asp Leu Ala			
85	90	95	
Gln Leu Pro Thr Glu Val Trp Pro Asn Gly Glu Leu Pro Ala Asp Leu			
100	105	110	
Ala Ser Arg Val Gln Pro Leu Phe Ser Thr Asp Phe Tyr Arg Glu Lys			
115	120	125	
Trp Leu Val Ala Val Asp Gly Ser Gln Ile Glu Ile Ala Leu Asp Gln			
130	135	140	
Gly Glu Val Lys Ala Gly Glu Phe Ala Glu Pro Ile Cys Glu Leu Glu			
145	150	155	160
Leu Glu Leu Leu Ser Gly Asp Thr Arg Ala Val Leu Lys Leu Ala Asn			
165	170	175	
Gln Leu Val Ser Gln Thr Gly Leu Arg Gln Gly Ser Leu Ser Lys Ala			
180	185	190	
Ala Arg Gly Tyr His Leu Ala Gln Gly Asn Pro Ala Arg Glu Ile Lys			
195	200	205	
Pro Thr Thr Ile Leu His Val Ala Ala Lys Ala Asp Val Glu Gln Gly			
210	215	220	
Leu Glu Ala Ala Leu Glu Leu Ala Leu Ala Gln Trp Gln Tyr His Glu			
225	230	235	240
Glu Leu Trp Val Arg Gly Asn Asp Ala Ala Lys Glu Gln Val Leu Ala			
245	250	255	
Ala Ile Ser Leu Val Arg His Thr Leu Met Leu Phe Gly Gly Ile Val			
260	265	270	
Pro Arg Lys Ala Ser Thr His Leu Arg Asp Leu Leu Thr Gln Cys Glu			
275	280	285	
Ala Thr Ile Ala Ser Ala Val Ser Ala Val Thr Ala Val Tyr Ser Thr			
290	295	300	
Glu Thr Ala Met Ala Lys Leu Ala Leu Thr Glu Trp Leu Val Ser Lys			
305	310	315	320
Ala Trp Gln Pro Phe Leu Asp Ala Lys Ala Gln Gly Lys Ile Ser Asp			
325	330	335	
Ser Phe Lys Arg Phe Ala Asp Ile His Leu Ser Arg His Ala Ala Glu			
340	345	350	

Leu Lys Ser Val Phe Cys Gln Pro Leu Gly Asp Arg Tyr Arg Asp Gln
 355 360 365
 Leu Pro Arg Leu Thr Arg Asp Ile Asp Ser Ile Leu Leu Leu Ala Gly
 370 375 380
 Tyr Tyr Asp Pro Val Val Ala Gln Ala Trp Leu Glu Asn Trp Gln Gly
 385 390 395 400
 Leu His His Ala Ile Ala Thr Gly Gln Arg Ile Glu Ile Glu His Phe
 405 410 415
 Arg Asn Glu Ala Asn Asn Gln Glu Pro Phe Trp Leu His Ser Gly Lys
 420 425 430
 Arg

<210> 328
 <211> 70
 <212> PRT
 <213> E. Coli

<400> 328
 Met Ser Gly Lys Met Thr Gly Ile Val Lys Trp Phe Asn Ala Asp Lys
 1 5 10 15
 Gly Phe Gly Phe Ile Thr Pro Asp Asp Gly Ser Lys Asp Val Phe Val
 20 25 30
 His Phe Ser Ala Ile Gln Asn Asp Gly Tyr Lys Ser Leu Asp Glu Gly
 35 40 45
 Gln Lys Val Ser Phe Thr Ile Glu Ser Gly Ala Lys Gly Pro Ala Ala
 50 55 60
 Gly Asn Val Thr Ser Leu
 65 70

<210> 329
 <211> 523
 <212> PRT
 <213> E. Coli

<400> 329
 Met Arg Asp Ile Val Asp Pro Val Phe Ser Ile Gly Ile Ser Ser Leu
 1 5 10 15
 Trp Asp Glu Leu Arg His Met Pro Ala Gly Gly Val Trp Trp Phe Asn
 20 25 30
 Val Asp Arg His Glu Asp Ala Ile Ser Leu Ala Asn Gln Thr Ile Ala
 35 40 45
 Ser Gln Ala Glu Thr Ala His Val Ala Val Ile Ser Met Asp Ser Asp
 50 55 60
 Pro Ala Lys Ile Phe Gln Leu Asp Asp Ser Gln Gly Pro Glu Lys Ile
 65 70 75 80
 Lys Leu Phe Ser Met Leu Asn His Glu Lys Gly Leu Tyr Tyr Leu Thr
 85 90 95
 Arg Asp Leu Gln Cys Ser Ile Asp Pro His Asn Tyr Leu Phe Ile Leu
 100 105 110
 Val Cys Ala Asn Asn Ala Trp Gln Asn Ile Pro Ala Glu Arg Leu Arg
 115 120 125
 Ser Trp Leu Asp Lys Met Asn Lys Trp Ser Arg Leu Asn His Cys Ser

130	135	140
Leu Leu Val Ile Asn Pro Gly Asn Asn Asn Asp Lys Gln Phe Ser Leu		
145	150	155
Leu Leu Glu Glu Tyr Arg Ser Leu Phe Gly Leu Ala Ser Leu Arg Phe		160
165	170	175
Gln Gly Asp Gln His Leu Leu Asp Ile Ala Phe Trp Cys Asn Glu Lys		
180	185	190
Gly Val Ser Ala Arg Gln Gln Leu Ser Val Gln Gln Asn Gly Ile		
195	200	205
Trp Thr Leu Val Gln Ser Glu Glu Ala Glu Ile Gln Pro Arg Ser Asp		
210	215	220
Glu Lys Arg Ile Leu Ser Asn Val Ala Val Leu Glu Gly Ala Pro Pro		
225	230	235
240		
Leu Ser Glu His Trp Gln Leu Phe Asn Asn Glu Val Leu Phe Asn		
245	250	255
Glu Ala Arg Thr Ala Gln Ala Ala Thr Val Val Phe Ser Leu Gln Gln		
260	265	270
Asn Ala Gln Ile Glu Pro Leu Ala Arg Ser Ile His Thr Leu Arg Arg		
275	280	285
Gln Arg Gly Ser Ala Met Lys Ile Leu Val Arg Glu Asn Thr Ala Ser		
290	295	300
Leu Arg Ala Thr Asp Glu Arg Leu Leu Leu Ala Cys Gly Ala Asn Met		
305	310	315
320		
Val Ile Pro Trp Asn Ala Pro Leu Ser Arg Cys Leu Thr Met Ile Glu		
325	330	335
Ser Val Gln Gly Gln Lys Phe Ser Arg Tyr Val Pro Glu Asp Ile Thr		
340	345	350
Thr Leu Leu Ser Met Thr Gln Pro Leu Lys Leu Arg Gly Phe Gln Lys		
355	360	365
Trp Asp Val Phe Cys Asn Ala Val Asn Asn Met Met Asn Asn Pro Leu		
370	375	380
Leu Pro Ala His Gly Lys Gly Val Leu Val Ala Leu Arg Pro Val Pro		
385	390	395
400		
Gly Ile Arg Val Glu Gln Ala Leu Thr Leu Cys Arg Pro Asn Arg Thr		
405	410	415
Gly Asp Ile Met Thr Ile Gly Gly Asn Arg Leu Val Leu Phe Leu Ser		
420	425	430
Phe Cys Arg Ile Asn Asp Leu Asp Thr Ala Leu Asn His Ile Phe Pro		
435	440	445
Leu Pro Thr Gly Asp Ile Phe Ser Asn Arg Met Val Trp Phe Glu Asp		
450	455	460
Asp Gln Ile Ser Ala Glu Leu Val Gln Met Arg Leu Leu Ala Pro Glu		
465	470	475
480		
Gln Trp Gly Met Pro Leu Pro Leu Thr Gln Ser Ser Lys Pro Val Ile		
485	490	495
Asn Ala Glu His Asp Gly Arg His Trp Arg Arg Ile Pro Glu Pro Met		
500	505	510
Arg Leu Leu Asp Asp Ala Val Glu Arg Ser Ser		
515	520	

<210> 330

<211> 62

<212> PRT

<213> E. Coli

<400> 330

Met	Thr	Ile	Ser	Asp	Ile	Ile	Glu	Ile	Ile	Val	Val	Cys	Ala	Leu	Ile
1					5				10						15
Phe	Phe	Pro	Leu	Gly	Tyr	Leu	Ala	Arg	His	Ser	Leu	Arg	Arg	Ile	Arg
					20				25						30
Asp	Thr	Leu	Arg	Leu	Phe	Phe	Ala	Lys	Pro	Arg	Tyr	Val	Lys	Pro	Ala
					35				40						45
Gly	Thr	Leu	Arg	Arg	Thr	Glu	Lys	Ala	Arg	Ala	Thr	Lys	Lys		
					50				55						60

<210> 331
<211> 559
<212> PRT
<213> E. Coli

<400> 331

Met	Thr	Gln	Phe	Thr	Gln	Asn	Thr	Ala	Met	Pro	Ser	Ser	Leu	Trp	Gln
1					5				10						15
Tyr	Trp	Arg	Gly	Leu	Ser	Gly	Trp	Asn	Phe	Tyr	Phe	Leu	Val	Lys	Phe
					20				25						30
Gly	Leu	Leu	Trp	Ala	Gly	Tyr	Leu	Asn	Phe	His	Pro	Leu	Leu	Asn	Leu
					35				40						45
Val	Phe	Ala	Ala	Phe	Leu	Leu	Met	Pro	Leu	Pro	Arg	Tyr	Ser	Leu	His
					50				55						60
Arg	Leu	Arg	His	Trp	Ile	Ala	Leu	Pro	Ile	Gly	Phe	Ala	Leu	Phe	Trp
					65				70						80
His	Asp	Thr	Trp	Leu	Pro	Gly	Pro	Glu	Ser	Ile	Met	Ser	Gln	Gly	Ser
					85				90						95
Gln	Val	Ala	Gly	Phe	Ser	Thr	Asp	Tyr	Leu	Ile	Asp	Leu	Val	Thr	Arg
					100				105						110
Phe	Ile	Asn	Trp	Gln	Met	Ile	Gly	Ala	Ile	Phe	Val	Leu	Leu	Val	Ala
					115				120						125
Trp	Leu	Phe	Leu	Ser	Gln	Trp	Ile	Arg	Ile	Thr	Val	Phe	Val	Val	Ala
					130				135						140
Ile	Leu	Leu	Trp	Leu	Asn	Val	Leu	Thr	Leu	Ala	Gly	Pro	Ser	Phe	Ser
					145				150						160
Leu	Trp	Pro	Ala	Gly	Gln	Pro	Thr	Thr	Thr	Val	Thr	Thr	Thr	Gly	Gly
					165				170						175
Asn	Ala	Ala	Ala	Thr	Val	Ala	Ala	Thr	Gly	Gly	Ala	Pro	Val	Val	Gly
					180				185						190
Asp	Met	Pro	Ala	Gln	Thr	Ala	Pro	Pro	Thr	Thr	Ala	Asn	Leu	Asn	Ala
					195				200						205
Trp	Leu	Asn	Asn	Phe	Tyr	Asn	Ala	Glu	Ala	Lys	Arg	Lys	Ser	Thr	Phe
					210				215						220
Pro	Ser	Ser	Leu	Pro	Ala	Asp	Ala	Gln	Pro	Phe	Glu	Leu	Leu	Val	Ile
					225				230						240
Asn	Ile	Cys	Ser	Leu	Ser	Trp	Ser	Asp	Ile	Glu	Ala	Ala	Gly	Leu	Met
					245				250						255
Ser	His	Pro	Leu	Trp	Ser	His	Phe	Asp	Ile	Glu	Phe	Lys	Asn	Phe	Asn
					260				265						270
Ser	Ala	Thr	Ser	Tyr	Ser	Gly	Pro	Ala	Ala	Ile	Arg	Leu	Leu	Arg	Ala
					275				280						285
Ser	Cys	Gly	Gln	Thr	Ser	His	Thr	Asn	Leu	Tyr	Gln	Pro	Ala	Asn	Asn
					290				295						300
Asp	Cys	Tyr	Leu	Phe	Asp	Asn	Leu	Ser	Lys	Leu	Gly	Phe	Thr	Gln	His
					305				310						320
Leu	Met	Met	Gly	His	Asn	Gly	Gln	Phe	Gly	Gly	Phe	Leu	Lys	Glu	Val

	325	330	335
Arg Glu Asn Gly Gly Met Gln Ser Glu Leu Met Asp Gln Thr Asn Leu			
340	345	350	
Pro Val Ile Leu Leu Gly Phe Asp Gly Ser Pro Val Tyr Asp Asp Thr			
355	360	365	
Ala Val Leu Asn Arg Trp Leu Asp Val Thr Glu Lys Asp Lys Asn Ser			
370	375	380	
Arg Ser Ala Thr Phe Tyr Asn Thr Leu Pro Leu His Asp Gly Asn His			
385	390	395	400
Tyr Pro Gly Val Ser Lys Thr Ala Asp Tyr Lys Ala Arg Ala Gln Lys			
405	410	415	
Phe Phe Asp Glu Leu Asp Ala Phe Phe Thr Glu Leu Glu Lys Ser Gly			
420	425	430	
Arg Lys Val Met Val Val Val Pro Glu His Gly Gly Ala Leu Lys			
435	440	445	
Gly Asp Arg Met Gln Val Ser Gly Leu Arg Asp Ile Pro Ser Pro Ser			
450	455	460	
Ile Thr Asp Val Pro Val Gly Val Lys Phe Phe Gly Met Lys Ala Pro			
465	470	475	480
His Gln Gly Ala Pro Ile Val Ile Glu Gln Pro Ser Ser Phe Leu Ala			
485	490	495	
Ile Ser Asp Leu Val Val Arg Val Leu Asp Gly Lys Ile Phe Thr Glu			
500	505	510	
Asp Asn Val Asp Trp Lys Lys Leu Thr Ser Gly Leu Pro Gln Thr Ala			
515	520	525	
Pro Val Ser Glu Asn Ser Asn Ala Val Val Ile Gln Tyr Gln Asp Lys			
530	535	540	
Pro Tyr Val Arg Leu Asn Gly Gly Asp Trp Val Pro Tyr Pro Gln			
545	550	555	

<210> 332

<211> 127

<212> PRT

<213> E. Coli

<400> 332

Met Glu Gly Ser Arg Met Lys Tyr Arg Ile Ala Leu Ala Val Ser Leu			
1	5	10	15
Phe Ala Leu Ser Ala Gly Ser Tyr Ala Thr Thr Leu Cys Gln Glu Lys			
20	25	30	
Glu Gln Asn Ile Leu Lys Glu Ile Ser Tyr Ala Glu Lys His Gln Asn			
35	40	45	
Gln Asn Arg Ile Asp Gly Leu Asn Lys Ala Leu Ser Glu Val Arg Ala			
50	55	60	
Asn Cys Ser Asp Ser Gln Leu Arg Ala Asp His Gln Lys Lys Ile Ala			
65	70	75	80
Lys Gln Lys Asp Glu Val Ala Glu Arg Gln Gln Asp Leu Ala Glu Ala			
85	90	95	
Lys Gln Lys Gly Asp Ala Asp Lys Ile Ala Lys Arg Glu Arg Lys Leu			
100	105	110	
Ala Glu Ala Gln Glu Glu Leu Lys Lys Leu Glu Ala Arg Asp Tyr			
115	120	125	

<210> 333

<211> 101

<212> PRT
<213> E. Coli

<400> 333

Met Ser Lys Glu His Thr Thr Glu His Leu Arg Ala Glu Leu Lys Ser
1 5 10 15
Leu Ser Asp Thr Leu Glu Glu Val Leu Ser Ser Ser Gly Glu Lys Ser
20 25 30
Lys Glu Glu Leu Ser Lys Ile Arg Ser Lys Ala Glu Gln Ala Leu Lys
35 40 45
Gln Ser Arg Tyr Arg Leu Gly Glu Thr Gly Asp Ala Ile Ala Lys Gln
50 55 60
Thr Arg Val Ala Ala Ala Arg Ala Asp Glu Tyr Val Arg Glu Asn Pro
65 70 75 80
Trp Thr Gly Val Gly Ile Gly Ala Ala Ile Gly Val Val Leu Gly Val
85 90 95
Leu Leu Ser Arg Arg
100

<210> 334

<211> 134

<212> PRT

<213> E. Coli

<400> 334

Met Ala Asp Thr His His Ala Gln Gly Pro Gly Lys Ser Val Leu Gly
1 5 10 15
Ile Gly Gln Arg Ile Val Ser Ile Met Val Glu Met Val Glu Thr Arg
20 25 30
Leu Arg Leu Ala Val Val Glu Leu Glu Glu Lys Ala Asn Leu Phe
35 40 45
Gln Leu Leu Leu Met Leu Gly Leu Thr Met Leu Phe Ala Ala Phe Gly
50 55 60
Leu Met Ser Leu Met Val Leu Ile Ile Trp Ala Val Asp Pro Gln Tyr
65 70 75 80
Arg Leu Asn Ala Met Ile Ala Thr Thr Val Val Leu Leu Leu Ala
85 90 95
Leu Ile Gly Gly Ile Trp Thr Leu Arg Lys Ser Arg Lys Ser Thr Leu
100 105 110
Leu Arg His Thr Arg His Glu Leu Ala Asn Asp Arg Gln Leu Leu Glu
115 120 125
Glu Glu Ser Arg Glu Gln
130

<210> 335

<211> 99

<212> PRT

<213> E. Coli

<400> 335

Met Ser Ser Lys Val Glu Arg Glu Arg Arg Lys Ala Gln Leu Leu Ser
1 5 10 15
Gln Ile Gln Gln Gln Arg Leu Asp Leu Ser Ala Ser Arg Arg Glu Trp
20 25 30

Leu Glu Thr Thr Gly Ala Tyr Asp Arg Arg Trp Asn Met Leu Leu Ser
 35 40 45
 Leu Arg Ser Trp Ala Leu Val Gly Ser Ser Val Met Ala Ile Trp Thr
 50 55 60
 Ile Arg His Pro Asn Met Leu Val Arg Trp Ala Arg Arg Gly Phe Gly
 65 70 75 80
 Val Trp Ser Ala Trp Arg Leu Val Lys Thr Thr Leu Lys Gln Gln Gln
 85 90 95
 Leu Arg Gly

<210> 336
 <211> 160
 <212> PRT
 <213> E. Coli

<400> 336
 Met Ile Leu Ser Ile Asp Ser Asn Asp Ala Asn Thr Ala Pro Leu His
 1 5 10 15
 Lys Lys Thr Ile Ser Ser Leu Ser Gly Ala Val Glu Ser Met Met Lys
 20 25 30
 Lys Leu Glu Asp Val Gly Val Leu Val Ala Arg Ile Leu Met Pro Ile
 35 40 45
 Leu Phe Ile Thr Ala Gly Trp Gly Lys Ile Thr Gly Tyr Ala Gly Thr
 50 55 60
 Gln Gln Tyr Met Glu Ala Met Gly Val Pro Gly Phe Met Leu Pro Leu
 65 70 75 80
 Val Ile Leu Leu Glu Phe Gly Gly Leu Ala Ile Leu Phe Gly Phe
 85 90 95
 Leu Thr Arg Thr Thr Ala Leu Phe Thr Ala Gly Phe Thr Leu Leu Thr
 100 105 110
 Ala Phe Leu Phe His Ser Asn Phe Ala Glu Gly Val Asn Ser Leu Met
 115 120 125
 Phe Met Lys Asn Leu Thr Ile Ser Gly Gly Phe Leu Leu Leu Ala Ile
 130 135 140
 Thr Gly Pro Gly Ala Tyr Ser Ile Asp Arg Leu Leu Asn Lys Lys Trp
 145 150 155 160

<210> 337
 <211> 296
 <212> PRT
 <213> E. Coli

<400> 337
 Met Ile Lys Lys Thr Thr Glu Ile Asp Ala Ile Leu Leu Asn Leu Asn
 1 5 10 15
 Lys Ala Ile Asp Ala His Tyr Gln Trp Leu Val Ser Met Phe His Ser
 20 25 30
 Val Val Ala Arg Asp Ala Ser Lys Pro Glu Ile Thr Asp Asn His Ser
 35 40 45
 Tyr Gly Leu Cys Gln Phe Gly Arg Trp Ile Asp His Leu Gly Pro Leu
 50 55 60
 Asp Asn Asp Glu Leu Pro Tyr Val Arg Leu Met Asp Ser Ala His Gln

65	70	75	80												
His	Met	His	Asn	Cys	Gly	Arg	Glu	Leu	Met	Leu	Ala	Ile	Val	Glu	Asn
				85					90						95
His	Trp	Gln	Asp	Ala	His	Phe	Asp	Ala	Phe	Gln	Glu	Gly	Leu	Leu	Ser
				100					105						110
Phe	Thr	Ala	Ala	Leu	Thr	Asp	Tyr	Lys	Ile	Tyr	Leu	Leu	Thr	Ile	Arg
				115					120						125
Ser	Asn	Met	Asp	Val	Leu	Thr	Gly	Leu	Pro	Gly	Arg	Arg	Val	Leu	Asp
				130					135						140
Glu	Ser	Phe	Asp	His	Gln	Leu	Arg	Asn	Ala	Glu	Pro	Leu	Asn	Leu	Tyr
				145					150						160
Leu	Met	Leu	Leu	Asp	Ile	Asp	Arg	Phe	Lys	Leu	Val	Asn	Asp	Thr	Tyr
				165					170						175
Gly	His	Leu	Ile	Gly	Asp	Val	Val	Leu	Arg	Thr	Leu	Ala	Thr	Tyr	Leu
				180					185						190
Ala	Ser	Trp	Thr	Arg	Asp	Tyr	Glu	Thr	Val	Tyr	Arg	Tyr	Gly	Gly	Glu
				195					200						205
Glu	Phe	Ile	Ile	Ile	Val	Lys	Ala	Ala	Asn	Asp	Glu	Glu	Ala	Cys	Arg
				210					215						220
Ala	Gly	Val	Arg	Ile	Cys	Gln	Leu	Val	Asp	Asn	His	Ala	Ile	Thr	His
				225					230						240
Ser	Glu	Gly	His	Ile	Asn	Ile	Thr	Val	Thr	Ala	Gly	Val	Ser	Arg	Ala
				245					250						255
Phe	Pro	Glu	Glu	Pro	Leu	Asp	Val	Val	Ile	Gly	Arg	Ala	Asp	Arg	Ala
				260					265						270
Met	Tyr	Glu	Gly	Lys	Gln	Thr	Gly	Arg	Asn	Arg	Cys	Met	Phe	Ile	Asp
				275					280						285
Glu	Gln	Asn	Val	Ile	Asn	Arg	Val								
				290					295						

<210> 338
<211> 203
<212> PRT
<213> E. Coli

<400> 338

Met	Arg	Leu	Arg	Val	Val	Pro	Gly	Phe	Ile	Ser	Pro	Pro	Gly	Phe	
1				5				10						15	
Gly	Gly	Leu	Gly	Tyr	Thr	Pro	Thr	Ala	Arg	Ala	Cys	Val	Asn	Ile	Ser
				20					25						30
Ile	Pro	Leu	Gln	Leu	Arg	Val	Ile	Asp	Met	Leu	Asp	Val	Phe	Thr	Pro
				35					40						45
Leu	Leu	Lys	Leu	Phe	Ala	Asn	Glu	Pro	Leu	Glu	Arg	Leu	Met	Tyr	Thr
				50					55						60
Ile	Ile	Ile	Phe	Gly	Leu	Thr	Leu	Trp	Leu	Ile	Pro	Lys	Glu	Phe	Thr
				65					70						80
Val	Ala	Phe	Asn	Ala	Tyr	Thr	Glu	Ile	Pro	Trp	Leu	Phe	Gln	Ile	Ile
				85					90						95
Val	Phe	Ala	Phe	Ser	Phe	Val	Val	Ala	Ile	Ser	Phe	Ser	Arg	Leu	Arg
				100					105						110
Ala	His	Ile	Gln	Lys	His	Tyr	Ser	Leu	Leu	Pro	Glu	Gln	Arg	Val	Leu
				115					120						125
Leu	Arg	Leu	Ser	Glu	Lys	Glu	Ile	Ala	Val	Phe	Lys	Asp	Phe	Leu	Lys
				130					135						140
Thr	Gly	Asn	Leu	Ile	Ile	Thr	Ser	Pro	Cys	Arg	Asn	Pro	Val	Met	Lys

145	150	155	160
Lys Leu Glu Arg Lys Gly Ile Ile Gln His Gln Ser Asp Ser Ala Asn			
165	170	175	
Cys Ser Tyr Tyr Leu Val Thr Glu Lys Tyr Ser His Phe Met Lys Leu			
180	185	190	
Phe Trp Asn Ser Arg Ser Arg Arg Phe Asn Arg			
195	200		

<210> 339
<211> 58
<212> PRT
<213> E. Coli

<400> 339

Met Leu Leu Gln Pro Ser Ala Arg Thr Ser Phe Gly Phe Lys Cys Phe			
1	5	10	15
Ala Phe Gly Ile Arg His Gly Ser Glu Arg Ser Ile Leu Val Gly Glu			
20	25	30	
His Ala Ala His Gln Gly Phe Val Val Ala Glu Val Asp Phe Leu His			
35	40	45	
Phe Ala Asn Leu Thr Ser Cys Cys Tyr Val			
50	55		

<210> 340
<211> 1426
<212> PRT
<213> E. Coli

<400> 340

Met Ser Gly Lys Pro Ala Ala Arg Gln Gly Asp Met Thr Gln Tyr Gly			
1	5	10	15
Gly Pro Ile Val Gln Gly Ser Ala Gly Val Arg Ile Gly Ala Pro Thr			
20	25	30	
Gly Val Ala Cys Ser Val Cys Pro Gly Gly Met Thr Ser Gly Asn Pro			
35	40	45	
Val Asn Pro Leu Leu Gly Ala Lys Val Leu Pro Gly Glu Thr Asp Leu			
50	55	60	
Ala Leu Pro Gly Pro Leu Pro Phe Ile Leu Ser Arg Thr Tyr Ser Ser			
65	70	75	80
Tyr Arg Thr Lys Thr Pro Ala Pro Val Gly Val Phe Gly Pro Gly Trp			
85	90	95	
Lys Ala Pro Ser Asp Ile Arg Leu Gln Leu Arg Asp Asp Gly Leu Ile			
100	105	110	
Leu Asn Asp Asn Gly Gly Arg Ser Ile His Phe Glu Pro Leu Leu Pro			
115	120	125	
Gly Glu Ala Val Tyr Ser Arg Ser Glu Ser Met Trp Leu Val Arg Gly			
130	135	140	
Gly Lys Ala Ala Gln Pro Asp Gly His Thr Leu Ala Arg Leu Trp Gly			
145	150	155	160
Ala Leu Pro Pro Asp Ile Arg Leu Ser Pro His Leu Tyr Leu Ala Thr			
165	170	175	
Asn Ser Ala Gln Gly Pro Trp Trp Ile Leu Gly Trp Ser Glu Arg Val			
180	185	190	
Pro Gly Ala Glu Asp Val Leu Pro Ala Pro Leu Pro Pro Tyr Arg Val			

195	200	205
Leu Thr Gly Met Ala Asp Arg Phe	Gly Arg Thr Leu	Thr Tyr Arg Arg
210	215	220
Glu Ala Ala Gly Asp Leu Ala Gly Glu Ile	Thr Gly Val Thr Asp Gly	
225	230	235
Ala Gly Arg Glu Phe Arg Leu Val Leu	Thr Thr Gln Ala Gln Arg Ala	
245	250	255
Glu Glu Ala Arg Thr Ser Ser Leu Ser Ser Ser Asp Ser Ser Arg Pro		
260	265	270
Leu Ser Ala Ser Ala Phe Pro Asp Thr Leu Pro Gly Thr	Glu Tyr Gly	
275	280	285
Pro Asp Arg Gly Ile Arg Leu Ser Ala Val Trp	Leu Met His Asp Pro	
290	295	300
Ala Tyr Pro Glu Ser Leu Pro Ala Ala Pro	Leu Val Arg Tyr Thr Tyr	
305	310	315
Thr Glu Ala Gly Glu Leu Leu Ala Val	Tyr Asp Arg Ser Asn Thr Gln	
325	330	335
Val Arg Ala Phe Thr Tyr Asp Ala Gln His Pro	Gly Arg Met Val Ala	
340	345	350
His Arg Tyr Ala Gly Arg Pro Glu Met Arg Tyr Arg Tyr Asp Asp Thr		
355	360	365
Gly Arg Val Val Glu Gln Leu Asn Pro Ala Gly	Leu Ser Tyr Arg Tyr	
370	375	380
Leu Tyr Glu Gln Asp Arg Ile Thr Val Thr Asp	Ser Leu Asn Arg Arg	
385	390	395
Glu Val Leu His Thr Glu Gly Gly Ala Gly	Leu Lys Arg Val Val Lys	
405	410	415
Lys Glu Leu Ala Asp Gly Ser Val Thr Arg Ser Gly	Tyr Asp Ala Ala	
420	425	430
Gly Arg Leu Thr Ala Gln Thr Asp Ala Ala Gly Arg Arg	Arg Thr Glu Tyr	
435	440	445
Gly Leu Asn Val Val Ser Gly Asp Ile Thr Asp	Ile Thr Thr Pro Asp	
450	455	460
Gly Arg Glu Thr Lys Phe Tyr Tyr Asn Asp Gly Asn Gln	Leu Thr Ala	
465	470	475
Val Val Ser Pro Asp Gly Leu Glu Ser Arg Arg	Glu Tyr Asp Glu Pro	
485	490	495
Gly Arg Leu Val Ser Glu Thr Ser Arg Ser Gly	Glu Thr Val Arg Tyr	
500	505	510
Arg Tyr Asp Asp Ala His Ser Glu Leu Pro Ala	Thr Thr Asp Ala	
515	520	525
Thr Gly Ser Thr Arg Gln Met Thr Trp Ser Arg	Tyr Gly Gln Leu Leu	
530	535	540
Ala Phe Thr Asp Cys Ser Gly Tyr Gln Thr Arg	Tyr Glu Tyr Asp Arg	
545	550	555
Phe Gly Gln Met Thr Ala Val His Arg Glu Glu	Gly Ile Ser Leu Tyr	
565	570	575
Arg Arg Tyr Asp Asn Arg Gly Arg Leu Thr Ser Val	Lys Asp Ala Gln	
580	585	590
Gly Arg Glu Thr Arg Tyr Glu Tyr Asn Ala Ala	Gly Asp Leu Thr Ala	
595	600	605
Val Ile Thr Pro Asp Gly Asn Arg Ser Glu Thr	Gln Tyr Asp Ala Trp	
610	615	620
Gly Lys Ala Val Ser Thr Thr Gln Gly Gly	Leu Thr Arg Ser Met Glu	
625	630	635
Tyr Asp Ala Ala Gly Arg Val Ile Ser Leu Thr	Asn Glu Asn Gly Ser	
645	650	655

His Ser Val Phe Ser Tyr Asp Ala Leu Asp Arg Leu Val Gln Gln Gly
 660 665 670
 Gly Phe Asp Gly Arg Thr Gln Arg Tyr His Tyr Asp Leu Thr Gly Lys
 675 680 685
 Leu Thr Gln Ser Glu Asp Glu Gly Leu Val Ile Leu Trp Tyr Tyr Asp
 690 695 700
 Glu Ser Asp Arg Ile Thr His Arg Thr Val Asn Gly Glu Pro Ala Glu
 705 710 715 720
 Gln Trp Gln Tyr Asp Gly His Gly Trp Leu Thr Asp Ile Ser His Leu
 725 730 735
 Ser Glu Gly His Arg Val Ala Val His Tyr Gly Tyr Asp Asp Lys Gly
 740 745 750
 Arg Leu Thr Gly Glu Cys Gln Thr Val Glu Asn Pro Glu Thr Gly Glu
 755 760 765
 Leu Leu Trp Gln His Glu Thr Lys His Ala Tyr Asn Glu Gln Gly Leu
 770 775 780
 Ala Asn Arg Val Thr Pro Asp Ser Leu Pro Pro Val Glu Trp Leu Thr
 785 790 795 800
 Tyr Gly Ser Gly Tyr Leu Ala Gly Met Lys Leu Gly Gly Thr Pro Leu
 805 810 815
 Val Glu Tyr Thr Arg Asp Arg Leu His Arg Glu Thr Val Arg Ser Phe
 820 825 830
 Gly Ser Met Ala Gly Ser Asn Ala Ala Tyr Glu Leu Thr Ser Thr Tyr
 835 840 845
 Thr Pro Ala Gly Gln Leu Gln Ser Gln His Leu Asn Ser Leu Val Tyr
 850 855 860
 Asp Arg Asp Tyr Gly Trp Ser Asp Asn Gly Asp Leu Val Arg Ile Ser
 865 870 875 880
 Gly Pro Arg Gln Thr Arg Glu Tyr Gly Tyr Ser Ala Thr Gly Arg Leu
 885 890 895
 Glu Ser Val Arg Thr Leu Ala Pro Asp Leu Asp Ile Arg Ile Pro Tyr
 900 905 910
 Ala Thr Asp Pro Ala Gly Asn Arg Leu Pro Asp Pro Glu Leu His Pro
 915 920 925
 Asp Ser Thr Leu Thr Val Trp Pro Asp Asn Arg Ile Ala Glu Asp Ala
 930 935 940
 His Tyr Val Tyr Arg His Asp Glu Tyr Gly Arg Leu Thr Glu Lys Thr
 945 950 955 960
 Asp Arg Ile Pro Ala Gly Val Ile Arg Thr Asp Asp Glu Arg Thr His
 965 970 975
 His Tyr His Tyr Asp Ser Gln His Arg Leu Val Phe Tyr Thr Arg Ile
 980 985 990
 Gln His Gly Glu Pro Leu Val Glu Ser Arg Tyr Leu Tyr Asp Pro Leu
 995 1000 1005
 Gly Arg Arg Met Ala Lys Arg Val Trp Arg Arg Glu Arg Asp Leu Thr
 1010 1015 1020
 Gly Trp Met Ser Leu Ser Arg Lys Pro Glu Val Thr Trp Tyr Gly Trp
 1025 1030 1035 1040
 Asp Gly Asp Arg Leu Thr Thr Val Gln Thr Asp Thr Thr Arg Ile Gln
 1045 1050 1055
 Thr Val Tyr Glu Pro Gly Ser Phe Thr Pro Leu Ile Arg Val Glu Thr
 1060 1065 1070
 Glu Asn Gly Glu Arg Glu Lys Ala Gln Arg Arg Ser Leu Ala Glu Thr
 1075 1080 1085
 Leu Gln Gln Glu Gly Ser Glu Asn Gly His Gly Val Val Phe Pro Ala
 1090 1095 1100
 Glu Leu Val Arg Leu Leu Asp Arg Leu Glu Glu Ile Arg Ala Asp

1105	1110	1115	1120
Arg Val Ser Ser Glu Ser Arg Ala Trp Leu Ala Gln Cys Gly Leu Thr			
1125	1130	1135	
Val Glu Gln Leu Ala Arg Gln Val Glu Pro Glu Tyr Thr Pro Ala Arg			
1140	1145	1150	
Lys Ala His Leu Tyr His Cys Asp His Arg Gly Leu Pro Leu Ala Leu			
1155	1160	1165	
Ile Ser Glu Asp Gly Asn Thr Ala Trp Ser Ala Glu Tyr Asp Glu Trp			
1170	1175	1180	
Gly Asn Gln Leu Asn Glu Glu Asn Pro His His Val Tyr Gln Pro Tyr			
1185	1190	1195	1200
Arg Leu Pro Gly Gln Gln His Asp Glu Glu Ser Gly Leu Tyr Tyr Asn			
1205	1210	1215	
Arg His Arg Tyr Tyr Asp Pro Leu Gln Gly Arg Tyr Ile Thr Gln Asp			
1220	1225	1230	
Pro Met Gly Leu Lys Gly Gly Trp Asn Leu Tyr Gln Tyr Pro Leu Asn			
1235	1240	1245	
Pro Leu Gln Gln Ile Asp Pro Met Gly Leu Leu Gln Thr Trp Asp Asp			
1250	1255	1260	
Ala Arg Ser Gly Ala Cys Thr Gly Gly Val Cys Gly Val Leu Ser Arg			
1265	1270	1275	1280
Ile Ile Gly Pro Ser Lys Phe Asp Ser Thr Ala Asp Ala Ala Leu Asp			
1285	1290	1295	
Ala Leu Lys Glu Thr Gln Asn Arg Ser Leu Cys Asn Asp Met Glu Tyr			
1300	1305	1310	
Ser Gly Ile Val Cys Lys Asp Thr Asn Gly Lys Tyr Phe Ala Ser Lys			
1315	1320	1325	
Ala Glu Thr Asp Asn Leu Arg Lys Glu Ser Tyr Pro Leu Lys Arg Lys			
1330	1335	1340	
Cys Pro Thr Gly Thr Asp Arg Val Ala Ala Tyr His Thr His Gly Ala			
1345	1350	1355	1360
Asp Ser His Gly Asp Tyr Val Asp Glu Phe Phe Ser Ser Ser Asp Lys			
1365	1370	1375	
Asn Leu Val Arg Ser Lys Asp Asn Asn Leu Glu Ala Phe Tyr Leu Ala			
1380	1385	1390	
Thr Pro Asp Gly Arg Phe Glu Ala Leu Asn Asn Lys Gly Glu Tyr Ile			
1395	1400	1405	
Phe Ile Arg Asn Ser Val Pro Gly Leu Ser Ser Val Cys Ile Pro Tyr			
1410	1415	1420	
His Asp			
1425			

<210> 341
<211> 122
<212> PRT
<213> E. Coli

<400> 341

Met Lys Tyr Ser Ser Ile Phe Ser Met Leu Ser Phe Phe Ile Leu Phe			
1	5	10	15
Ala Cys Asn Glu Thr Ala Val Tyr Gly Ser Asp Glu Asn Ile Ile Phe			
20	25	30	
Met Arg Tyr Val Glu Lys Leu His Leu Asp Lys Tyr Ser Val Lys Asn			
35	40	45	
Thr Val Lys Thr Glu Thr Met Ala Ile Gln Leu Ala Glu Ile Tyr Val			
50	55	60	

Arg	Tyr	Arg	Tyr	Gly	Glu	Arg	Ile	Ala	Glu	Glu	Lys	Pro	Tyr	Leu	
65				70					75				80		
Ile	Thr	Glu	Leu	Pro	Asp	Ser	Trp	Val	Val	Glu	Gly	Ala	Lys	Leu	Pro
				85					90				95		
Tyr	Glu	Val	Ala	Gly	Gly	Val	Phe	Ile	Ile	Glu	Ile	Asn	Lys	Lys	Asn
				100					105				110		
Gly	Cys	Val	Leu	Asn	Phe	Leu	His	Ser	Lys						
				115					120						

<210> 342
<211> 236
<212> PRT
<213> E. Coli

<400> 342

Met	Leu	Ala	Leu	Met	Asp	Ala	Asp	Gly	Asn	Ile	Ala	Trp	Ser	Gly	Glu	
1				5					10				15			
Tyr	Asp	Glu	Trp	Gly	Asn	Gln	Leu	Asn	Glu	Glu	Asn	Pro	His	His	Leu	
				20					25				30			
His	Gln	Pro	Tyr	Arg	Leu	Pro	Gly	Gln	Gln	Tyr	Asp	Lys	Glu	Ser	Gly	
				35					40				45			
Leu	Tyr	Tyr	Asn	Arg	Asn	Arg	Tyr	Tyr	Asp	Pro	Leu	Gln	Gly	Arg	Tyr	
				50					55				60			
Ile	Thr	Gln	Asp	Pro	Ile	Gly	Leu	Glu	Gly	Gly	Trp	Ser	Leu	Tyr	Ala	
				65					70				75		80	
Tyr	Pro	Leu	Asn	Pro	Val	Asn	Gly	Ile	Asp	Pro	Leu	Gly	Leu	Ser	Pro	
					85					90				95		
Ala	Asp	Val	Ala	Leu	Ile	Arg	Arg	Lys	Asp	Gln	Leu	Asn	His	Gln	Arg	
					100					105				110		
Ala	Trp	Asp	Ile	Leu	Ser	Asp	Thr	Tyr	Glu	Asp	Met	Lys	Arg	Leu	Asn	
					115					120				125		
Leu	Gly	Gly	Thr	Asp	Gln	Phe	Phe	His	Cys	Met	Ala	Phe	Cys	Arg	Val	
					130					135				140		
Ser	Lys	Leu	Asn	Asp	Ala	Gly	Val	Ser	Arg	Ser	Ala	Lys	Gly	Leu	Gly	
					145					150				155		160
Tyr	Glu	Lys	Glu	Ile	Arg	Asp	Tyr	Gly	Leu	Asn	Leu	Phe	Gly	Met	Tyr	
						165				170				175		
Gly	Arg	Lys	Val	Lys	Leu	Ser	His	Ser	Glu	Met	Ile	Glu	Asp	Asn	Lys	
						180				185				190		
Lys	Asp	Leu	Ala	Val	Asn	Asp	His	Gly	Leu	Thr	Cys	Pro	Ser	Thr	Thr	
						195				200				205		
Asp	Cys	Ser	Asp	Arg	Cys	Ser	Asp	Tyr	Ile	Asn	Pro	Glu	His	Lys	Lys	
						210				215				220		
Thr	Ile	Lys	Ala	Leu	Gln	Asp	Ala	Gly	Tyr	Leu	Lys					
					225					230				235		

<210> 343
<211> 86
<212> PRT
<213> E. Coli

<400> 343

Met	Leu	Ala	Ile	Ser	Ser	Asn	Leu	Ser	Lys	Met	Ile	Ile	Phe	Ile	Phe
1				5					10				15		
Ala	Ile	Ile	Ile	Ile	Val	Val	Leu	Cys	Val	Ile	Thr	Tyr	Leu	Tyr	Leu

20	25	30
Tyr Lys Asp Glu Ser Leu Val Ser Lys His Tyr Ile Asn Tyr Met Ala		
35	40	45
Ile Pro Glu Asn Asp Gly Val Phe Thr Trp Leu Pro Asp Phe Phe Pro		
50	55	60
His Val Ala Val Asp Ile Ser Ile Tyr Thr Asn Val Glu Asp Asp Tyr		
65	70	75
Phe Phe Leu Ile Phe Pro		
85		

<210> 344

<211> 63

<212> PRT

<213> E. Coli

<400> 344

Met Arg Ala Arg Glu Gln Val Ala Lys Ile Val Ser Lys Asn Asp Pro			
1	5	10	15
Asp Thr Lys Lys Val Trp Cys Lys Tyr Gly Lys Ile Pro Gly Gln Gly			
20	25	30	
Asp Gly Val Asn Leu Phe Phe Val Gly Glu Ile Asn Val Thr His Tyr			
35	40	45	
Phe Ile Thr Asn Ile Gly Ala Gly Leu Pro Asp Ala Cys Ala Glu			
50	55	60	

<210> 345

<211> 167

<212> PRT

<213> E. Coli

<400> 345

Met Pro Gly Asn Ser Pro His Tyr Gly Arg Trp Pro Gln His Asp Phe			
1	5	10	15
Thr Ser Leu Lys Lys Leu Arg Pro Gln Ser Val Thr Ser Arg Ile Gln			
20	25	30	
Pro Gly Ser Asp Val Ile Val Cys Ala Glu Met Asp Glu Gln Trp Gly			
35	40	45	
Tyr Val Gly Ala Lys Ser Arg Gln Arg Trp Leu Phe Tyr Ala Tyr Asp			
50	55	60	
Ser Leu Arg Lys Thr Val Val Ala His Val Phe Gly Glu Arg Thr Met			
65	70	75	80
Ala Thr Leu Gly Arg Leu Met Ser Leu Leu Ser Pro Phe Asp Val Val			
85	90	95	
Ile Trp Met Thr Asp Gly Trp Pro Leu Tyr Glu Ser Arg Leu Lys Gly			
100	105	110	
Lys Leu His Val Ile Ser Lys Arg Tyr Thr Gln Arg Ile Glu Arg His			
115	120	125	
Asn Leu Asn Leu Arg Gln His Leu Ala Arg Leu Gly Arg Lys Ser Leu			
130	135	140	
Ser Phe Ser Lys Ser Val Glu Leu His Asp Lys Val Ile Gly His Tyr			
145	150	155	160
Leu Asn Ile Lys His Tyr Gln			
165			

<210> 346
<211> 91
<212> PRT
<213> E. Coli

<400> 346
Met Ala Ser Val Ser Ile Ser Cys Pro Ser Cys Ser Ala Thr Asp Gly
1 5 10 15
Val Val Arg Asn Gly Lys Ser Thr Ala Gly His Gln Arg Tyr Leu Cys
20 25 30
Ser His Cys Arg Lys Thr Trp Gln Leu Gln Phe Thr Tyr Thr Ala Ser
35 40 45
Gln Pro Gly Thr His Gln Lys Ile Ile Asp Met Ala Met Asn Gly Val
50 55 60
Gly Cys Arg Ala Thr Ala Arg Ile Met Gly Val Gly Leu Asn Thr Ile
65 70 75 80
Leu Arg His Leu Lys Asn Ser Gly Arg Ser Arg
85 90

<210> 347
<211> 138
<212> PRT
<213> E. Coli

<400> 347
Met Met Thr Lys Thr Gln Ile Asn Lys Leu Ile Lys Met Met Asn Asp
1 5 10 15
Leu Asp Tyr Pro Phe Glu Ala Pro Leu Lys Glu Ser Phe Ile Glu Ser
20 25 30
Ile Ile Gln Ile Glu Phe Asn Ser Asn Ser Thr Asn Cys Leu Glu Lys
35 40 45
Leu Cys Asn Glu Val Ser Ile Leu Phe Lys Asn Gln Pro Asp Tyr Leu
50 55 60
Thr Phe Leu Arg Ala Met Asp Gly Phe Glu Val Asn Gly Leu Arg Leu
65 70 75 80
Phe Ser Leu Ser Ile Pro Glu Pro Ser Val Lys Asn Leu Phe Ala Val
85 90 95
Asn Glu Phe Tyr Arg Asn Asn Asp Asp Phe Ile Asn Pro Asp Leu Gln
100 105 110
Glu Arg Leu Val Ile Gly Asp Tyr Ser Ile Ser Ile Phe Thr Tyr Asp
115 120 125
Ile Lys Gly Asp Ala Ala Asn Leu Leu Ile
130 135

<210> 348
<211> 392
<212> PRT
<213> E. Coli

<400> 348
Met Ser Asn Ile Val Tyr Leu Thr Val Thr Gly Glu Gln Gln Gly Ser
1 5 10 15

Ile Ser Ala Gly Cys Gly Thr Ser Glu Ser Thr Gly Asn Arg Trp Gln
 20 25 30
 Ser Gly His Glu Asp Glu Ile Phe Thr Phe Ser Leu Leu Asn Asn Ile
 35 40 45
 Asn Asn Thr Gly Leu Gly Ser Gln Phe His Gly Ile Thr Phe Cys Lys
 50 55 60
 Leu Ile Asp Lys Ser Thr Pro Leu Phe Ile Asn Ser Ile Asn Asn Asn
 65 70 75 80
 Glu Gln Leu Phe Met Gly Phe Asp Phe Tyr Arg Ile Asn Arg Phe Gly
 85 90 95
 Arg Leu Glu Lys Tyr Tyr Ile Gln Leu Arg Gly Ala Phe Leu Ser
 100 105 110
 Ala Ile His His Gln Ile Ile Glu Asn Gln Leu Asp Thr Glu Thr Ile
 115 120 125
 Thr Ile Ser Tyr Glu Phe Ile Leu Cys Gln His Leu Ile Ala Asn Thr
 130 135 140
 Glu Phe Ser Tyr Leu Ala Leu Pro Glu Asn Tyr Asn Arg Leu Phe Leu
 145 150 155 160
 Pro Asn Ser Lys Asn Gln Thr Asn Asn Arg Phe Lys Thr Leu Asn Ser
 165 170 175
 Lys Ala Ile Gly Arg Leu Leu Ala Ala Gly Gly Val Tyr Asn Gly Asn
 180 185 190
 Ile Glu Gly Phe Arg Asp Thr Ala Glu Lys Leu Gly Gly Asp Ala Ile
 195 200 205
 Lys Gly Tyr Asp Gln Ile Leu Asn Glu Lys Thr Ala Gly Ile Ala Ile
 210 215 220
 Ala Thr Ala Ser Ile Leu Leu Thr Lys Arg Ser Asn Val Asp Thr Tyr
 225 230 235 240
 Thr Glu Ile Asn Ser Tyr Leu Gly Lys Leu Arg Gly Gln Gln Lys Leu
 245 250 255
 Leu Asp Gly Ile Asp Ile Ile Glu Ile Ile Tyr Ile Lys Arg Pro Ser
 260 265 270
 Lys Asp Leu Ala Asn Leu Arg Lys Glu Phe Asn Lys Thr Val Arg Lys
 275 280 285
 Asn Phe Leu Ile Lys Leu Ala Lys Thr Ser Glu Ala Ser Gly Arg Phe
 290 295 300
 Asn Ala Glu Asp Leu Leu Arg Met Arg Lys Gly Asn Val Pro Leu Asn
 305 310 315 320
 Tyr Asn Val His His Lys Leu Ser Leu Asp Asp Gly Gly Thr Asn Asp
 325 330 335
 Phe Glu Asn Leu Val Leu Ile Glu Asn Glu Pro Tyr His Lys Val Phe
 340 345 350
 Thr Asn Met Gln Ser Arg Ile Ala Lys Gly Ile Leu Val Gly Glu Ser
 355 360 365
 Lys Ile Thr Pro Trp Ala Ile Pro Ser Gly Ser Ile Tyr Pro Pro Met
 370 375 380
 Lys Asn Ile Met Asp His Thr Lys
 385 390

<210> 349
 <211> 221
 <212> PRT
 <213> E. Coli

<400> 349

Met	Val	Leu	Ala	Leu	Asn	Tyr	Asn	Met	His	Gly	Val	Asn	Ile	Arg	Ser
1				5					10					15	
Glu	Asn	Ala	Ala	Lys	Pro	His	Thr	Met	Pro	Ser	Arg	Tyr	Leu	Cys	Glu
				20				25					30		
Tyr	Ile	Arg	Ser	Ile	Glu	Lys	Asn	Gly	His	Ala	Leu	Asp	Phe	Gly	Cys
				35			40					45			
Gly	Lys	Leu	Arg	Tyr	Ser	Asp	Glu	Leu	Ile	Ser	Lys	Phe	Asp	Glu	Val
				50			55				60				
Thr	Phe	Leu	Asp	Ser	Lys	Arg	Gln	Leu	Glu	Arg	Glu	Gln	Ile	Ile	Arg
				65			70			75			80		
Gly	Ile	Lys	Thr	Lys	Ile	Ile	Asp	Tyr	Val	Pro	Arg	Tyr	Tyr	Lys	Asn
				85			90				95				
Ala	Asn	Thr	Val	Ala	Phe	Glu	Asp	Val	Asp	Lys	Ile	Ile	Gly	Gly	Tyr
				100			105					110			
Asp	Phe	Ile	Leu	Cys	Ser	Asn	Val	Leu	Ser	Ala	Val	Pro	Cys	Arg	Asp
				115			120					125			
Thr	Ile	Asp	Lys	Ile	Val	Leu	Ser	Ile	Lys	Arg	Leu	Leu	Lys	Ser	Gly
				130			135				140				
Gly	Glu	Thr	Leu	Ile	Val	Asn	Gln	Tyr	Lys	Ser	Ser	Tyr	Phe	Lys	Lys
				145			150			155			160		
Tyr	Glu	Thr	Gly	Arg	Lys	His	Leu	Tyr	Gly	Tyr	Ile	Tyr	Lys	Asn	Ser
				165			170				175				
Lys	Ser	Val	Ser	Tyr	Tyr	Gly	Leu	Leu	Asp	Glu	Leu	Ala	Val	Gln	Glu
				180			185				190				
Ile	Cys	Ser	Ser	His	Gly	Leu	Glu	Ile	Leu	Lys	Ser	Trp	Ser	Lys	Ala
				195			200				205				
Gly	Ser	Ser	Tyr	Val	Thr	Val	Gly	Ser	Cys	Asn	Ala	Ile			
				210			215				220				

<210> 350

<211> 234

. <212> PRT

. <213> E. Coli

<400> 350

Met	Asn	Asn	Met	Phe	Glu	Pro	Pro	Lys	Asn	Tyr	Asn	Glu	Met	Leu	Pro
1			5			10							15		
Lys	Leu	His	Lys	Ala	Thr	Phe	Leu	Asn	Thr	Leu	Ile	Tyr	Cys	Ile	Leu
				20			25				30				
Leu	Val	Ile	Tyr	Glu	Tyr	Ile	Pro	Leu	Ile	Thr	Leu	Pro	Thr	Lys	Tyr
				35			40				45				
Val	Pro	Pro	Ile	Lys	Asp	His	Glu	Ser	Phe	Ile	Asn	Trp	Ala	Leu	Ser
				50			55				60				
Phe	Gly	Ile	Leu	Pro	Cys	Ala	Phe	Ala	Ile	Phe	Ala	Tyr	Leu	Ile	Ser
				65			70			75			80		
Gly	Ala	Leu	Asp	Leu	His	Asn	Asn	Ala	Ala	Lys	Leu	Leu	Arg	Val	Arg
					85			90				95			
Tyr	Leu	Trp	Asp	Lys	His	Leu	Ile	Ile	Lys	Pro	Leu	Ser	Arg	Arg	Ala
				100			105				110				
Gly	Val	Asn	Arg	Lys	Leu	Asn	Lys	Asp	Glu	Ala	His	Asn	Val	Met	Ser
				115			120				125				
Asn	Leu	Tyr	Tyr	Pro	Glu	Val	Arg	Lys	Ile	Glu	Asp	Lys	His	Tyr	Ile
				130			135				140				
Glu	Leu	Phe	Trp	Asn	Lys	Val	Tyr	Tyr	Phe	Trp	Ile	Phe	Phe	Glu	Phe
				145			150				155			160	
Ser	Ile	Ile	Ala	Leu	Ile	Ser	Phe	Leu	Ile	Ile	Phe	Phe	Cys	Lys	Gln

	165	170	175												
Met	Asp	Ile	Phe	His	Val	Glu	Gly	Ser	Leu	Leu	Ser	Leu	Phe	Phe	Phe
	180		185										190		
Val	Ile	Leu	Ser	Phe	Ser	Val	Ser	Gly	Ile	Ile	Phe	Ala	Leu	Thr	Val
	195		200									205			
Lys	Pro	Arg	Thr	Glu	Ser	Gln	Val	Gly	Lys	Ile	Pro	Asp	Asp	Lys	Ile
	210		215								220				
Lys	Glu	Phe	Phe	Thr	Lys	Asn	Asn	Ile	Asn						
	225		230												

<210> 351
<211> 94
<212> PRT
<213> E. Coli

<400> 351

Met	Phe	Thr	Ile	Asn	Ala	Glu	Val	Arg	Lys	Glu	Gln	Gly	Lys	Gly	Ala
1				5					10				15		
Ser	Arg	Arg	Leu	Arg	Ala	Ala	Asn	Lys	Phe	Pro	Ala	Ile	Ile	Tyr	Gly
					20				25				30		
Gly	Lys	Glu	Ala	Pro	Leu	Ala	Ile	Glu	Leu	Asp	His	Asp	Lys	Val	Met
					35			40				45			
Asn	Met	Gln	Ala	Lys	Ala	Glu	Phe	Tyr	Ser	Glu	Val	Leu	Thr	Ile	Val
					50			55			60				
Val	Asp	Gly	Lys	Glu	Ile	Lys	Val	Lys	Ala	Gln	Asp	Val	Gln	Arg	His
					65			70			75			80	
Pro	Tyr	Lys	Pro	Lys	Leu	Gln	His	Ile	Asp	Phe	Val	Arg	Ala		
					85			90							

<210> 352
<211> 658
<212> PRT
<213> E. Coli

<400> 352

Met	Val	Leu	Phe	Tyr	Arg	Ala	His	Trp	Arg	Asp	Tyr	Lys	Asn	Asp	Gln
1				5					10				15		
Val	Arg	Ile	Met	Met	Asn	Leu	Thr	Thr	Leu	Thr	His	Arg	Asp	Ala	Leu
					20			25			30				
Cys	Leu	Asn	Ala	Arg	Phe	Thr	Ser	Arg	Glu	Glu	Ala	Ile	His	Ala	Leu
					35			40			45				
Thr	Gln	Arg	Leu	Ala	Ala	Leu	Gly	Lys	Ile	Ser	Ser	Thr	Glu	Gln	Phe
					50			55			60				
Leu	Glu	Glu	Val	Tyr	Arg	Arg	Glu	Ser	Leu	Gly	Pro	Thr	Ala	Leu	Gly
					65			70			75			80	
Glu	Gly	Leu	Ala	Val	Pro	His	Gly	Lys	Thr	Ala	Ala	Val	Lys	Glu	Ala
					85			90				95			
Ala	Phe	Ala	Val	Ala	Thr	Leu	Ser	Glu	Pro	Leu	Gln	Trp	Glu	Gly	Val
					100			105				110			
Asp	Gly	Pro	Glu	Ala	Val	Asp	Leu	Val	Val	Leu	Leu	Ala	Ile	Pro	Pro
					115			120				125			
Asn	Glu	Ala	Gly	Thr	Thr	His	Met	Gln	Leu	Leu	Thr	Ala	Leu	Thr	Thr
					130			135			140				
Arg	Leu	Ala	Asp	Asp	Glu	Ile	Arg	Ala	Arg	Ile	Gln	Ser	Ala	Thr	Thr

145	150	155	160												
Pro	Asp	Glu	Leu	Leu	Ser	Ala	Leu	Asp	Asp	Lys	Gly	Gly	Thr	Gln	Pro
165										170				175	
Ser	Ala	Ser	Phe	Ser	Asn	Ala	Pro	Thr	Ile	Val	Cys	Val	Thr	Ala	Cys
180										185				190	
Pro	Ala	Gly	Ile	Ala	His	Thr	Tyr	Met	Ala	Ala	Glu	Tyr	Leu	Glu	Lys
195										200				205	
Ala	Gly	Arg	Lys	Leu	Gly	Val	Asn	Val	Tyr	Val	Glu	Lys	Gln	Gly	Ala
210						215					220				
Asn	Gly	Ile	Glu	Gly	Arg	Leu	Thr	Ala	Asp	Gln	Leu	Asn	Ser	Ala	Thr
225						230				235				240	
Ala	Cys	Ile	Phe	Ala	Ala	Glu	Val	Ala	Ile	Lys	Glu	Ser	Glu	Arg	Phe
245										250				255	
Asn	Gly	Ile	Pro	Ala	Leu	Ser	Val	Pro	Val	Ala	Glu	Pro	Ile	Arg	His
260								265					270		
Ala	Glu	Ala	Leu	Ile	Gln	Gln	Ala	Leu	Thr	Leu	Lys	Arg	Ser	Asp	Glu
275								280					285		
Thr	Arg	Thr	Val	Gln	Gln	Asp	Thr	Gln	Pro	Val	Lys	Ser	Val	Lys	Thr
290							295				300				
Glu	Leu	Lys	Gln	Ala	Leu	Leu	Ser	Gly	Ile	Ser	Phe	Ala	Val	Pro	Leu
305						310				315				320	
Ile	Val	Ala	Gly	Gly	Thr	Val	Leu	Ala	Val	Ala	Val	Leu	Leu	Ser	Gln
								325		330				335	
Ile	Phe	Gly	Leu	Gln	Asp	Leu	Phe	Asn	Glu	Glu	Asn	Ser	Trp	Leu	Trp
						340			345				350		
Met	Tyr	Arg	Lys	Leu	Gly	Gly	Gly	Leu	Leu	Gly	Ile	Leu	Met	Val	Pro
								355		360			365		
Val	Leu	Ala	Ala	Tyr	Thr	Ala	Tyr	Ser	Leu	Ala	Asp	Lys	Pro	Ala	Leu
						370			375			380			
Ala	Pro	Gly	Phe	Ala	Ala	Gly	Leu	Ala	Ala	Asn	Met	Ile	Gly	Ser	Gly
						385			390			395			400
Phe	Leu	Gly	Ala	Val	Val	Gly	Gly	Leu	Ile	Ala	Gly	Tyr	Leu	Met	Arg
							405			410			415		
Trp	Val	Lys	Asn	His	Leu	Arg	Leu	Ser	Ser	Lys	Phe	Asn	Gly	Phe	Leu
						420			425			430			
Thr	Phe	Tyr	Leu	Tyr	Pro	Val	Leu	Gly	Thr	Leu	Gly	Ala	Gly	Ser	Leu
							435			440			445		
Met	Leu	Phe	Val	Val	Gly	Glu	Pro	Val	Ala	Trp	Ile	Asn	Asn	Ser	Leu
							450			455			460		
Thr	Ala	Trp	Leu	Asn	Gly	Leu	Ser	Gly	Ser	Asn	Ala	Leu	Leu	Gly	
						465			470			475			480
Ala	Ile	Leu	Gly	Phe	Met	Cys	Ser	Phe	Asp	Leu	Gly	Gly	Pro	Val	Asn
							485			490			495		
Lys	Ala	Ala	Tyr	Ala	Phe	Cys	Leu	Gly	Ala	Met	Ala	Asn	Gly	Val	Tyr
							500			505			510		
Gly	Pro	Tyr	Ala	Ile	Phe	Ala	Ser	Val	Lys	Met	Val	Ser	Ala	Phe	Thr
							515			520			525		
Val	Thr	Ala	Ser	Thr	Met	Leu	Ala	Pro	Arg	Leu	Phe	Lys	Glu	Phe	Glu
							530			535			540		
Ile	Glu	Thr	Gly	Lys	Ser	Thr	Trp	Leu	Leu	Gly	Leu	Ala	Gly	Ile	Thr
							545			550			555		
Glu	Gly	Ala	Ile	Pro	Met	Ala	Ile	Glu	Asp	Pro	Leu	Arg	Val	Ile	Gly
								565			570			575	
Ser	Phe	Val	Leu	Gly	Ser	Met	Val	Thr	Gly	Ala	Ile	Val	Gly	Ala	Met
								580			585			590	
Asn	Ile	Gly	Leu	Ser	Thr	Pro	Gly	Ala	Gly	Ile	Phe	Ser	Leu	Phe	Leu
								595			600			605	

Leu His Asp Asn Gly Ala Gly Gly Val Met Ala Ala Ile Gly Trp Phe
 610 615 620
 Gly Ala Ala Leu Val Gly Ala Ala Ile Ser Thr Ala Ile Leu Leu Met
 625 630 635 640
 Trp Arg Arg His Ala Val Lys His Gly Asn Tyr Leu Thr Asp Gly Val
 645 650 655
 Met Pro

<210> 353
 <211> 877
 <212> PRT
 <213> E. Coli

<400> 353
 Met Lys Ala Val Ser Arg Val His Ile Thr Pro His Met His Trp Asp
 1 5 10 15
 Arg Glu Trp Tyr Phe Thr Thr Glu Glu Ser Arg Ile Leu Leu Val Asn
 20 25 30
 Asn Met Glu Glu Ile Leu Cys Arg Leu Glu Gln Asn Glu Tyr Lys
 35 40 45
 Tyr Tyr Val Leu Asp Gly Gln Thr Ala Ile Leu Glu Asp Tyr Phe Ala
 50 55 60
 Val Lys Pro Glu Asn Lys Asp Arg Val Lys Lys Gln Val Glu Ala Gly
 65 70 75 80
 Lys Leu Ile Ile Gly Pro Trp Tyr Thr Gln Thr Asp Thr Thr Ile Val
 85 90 95
 Ser Ala Glu Ser Ile Val Arg Asn Leu Met Tyr Gly Met Arg Asp Cys
 100 105 110
 Leu Ala Phe Gly Glu Pro Met Lys Ile Gly Tyr Leu Pro Asp Ser Phe
 115 120 125
 Gly Met Ser Gly Gln Leu Pro His Ile Tyr Asn Gly Phe Gly Ile Thr
 130 135 140
 Arg Thr Met Phe Trp Arg Gly Cys Ser Glu Arg His Gly Thr Asp Lys
 145 150 155 160
 Thr Glu Phe Leu Trp Gln Ser Ser Asp Gly Ser Glu Val Thr Ala Gln
 165 170 175
 Val Leu Pro Leu Gly Tyr Ala Ile Gly Lys Tyr Leu Pro Ala Asp Glu
 180 185 190
 Asn Gly Leu Arg Lys Arg Leu Asp Ser Tyr Phe Asp Val Leu Glu Lys
 195 200 205
 Ala Ser Val Thr Lys Glu Ile Leu Leu Pro Asn Gly His Asp Gln Met
 210 215 220
 Pro Leu Gln Gln Asn Ile Phe Glu Val Met Asp Lys Leu Arg Glu Ile
 225 230 235 240
 Tyr Pro Gln Arg Lys Phe Val Met Ser Arg Phe Glu Glu Val Phe Glu
 245 250 255
 Lys Ile Glu Ala Gln Arg Asp Asn Leu Ala Thr Leu Lys Gly Glu Phe
 260 265 270
 Ile Asp Gly Lys Tyr Met Arg Val His Arg Thr Ile Gly Ser Thr Arg
 275 280 285
 Met Asp Ile Lys Ile Ala His Ala Arg Ile Glu Asn Lys Ile Val Asn
 290 295 300
 Leu Leu Glu Pro Leu Ala Thr Leu Ala Trp Thr Leu Gly Phe Glu Tyr
 305 310 315 320
 His His Gly Leu Leu Glu Lys Met Trp Lys Glu Ile Leu Lys Asn His

	325	330	335
Ala His Asp Ser Ile Gly Cys Cys Ser Asp Lys Val His Arg Glu			
340	345	350	
Ile Val Ala Arg Phe Glu Leu Ala Glu Asp Met Ala Asp Asn Leu Ile			
355	360	365	
Arg Phe Tyr Met Arg Lys Ile Ala Asp Asn Met Pro Gln Ser Asp Ala			
370	375	380	
Asp Lys Leu Val Leu Phe Asn Leu Met Pro Trp Pro Arg Glu Glu Val			
385	390	395	400
Ile Asn Thr Thr Val Arg Leu Arg Ala Ser Gln Phe Asn Leu Arg Asp			
405	410	415	
Asp Arg Gly Gln Pro Val Pro Tyr Phe Ile Arg His Ala Arg Glu Ile			
420	425	430	
Asp Pro Gly Leu Ile Asp Arg Gln Ile Val His Tyr Gly Asn Tyr Asp			
435	440	445	
Pro Phe Met Glu Phe Asp Ile Gln Ile Asn Gln Ile Val Pro Ser Met			
450	455	460	
Gly Tyr Arg Thr Leu Tyr Ile Glu Ala Asn Gln Pro Gly Asn Val Ile			
465	470	475	480
Ala Ala Lys Ser Asp Ala Glu Gly Ile Leu Glu Asn Ala Phe Trp Gln			
485	490	495	
Ile Ala Leu Asn Glu Asp Gly Ser Leu Gln Leu Val Asp Lys Asp Ser			
500	505	510	
Gly Val Arg Tyr Asp Arg Val Leu Gln Ile Glu Glu Ser Ser Asp Asp			
515	520	525	
Gly Asp Glu Tyr Asp Tyr Ser Pro Ala Lys Glu Glu Trp Val Ile Thr			
530	535	540	
Ala Ala Asn Ala Lys Pro Gln Cys Asp Ile Ile His Glu Ala Trp Gln			
545	550	555	560
Ser Arg Ala Val Ile Arg Tyr Asp Met Ala Val Pro Leu Asn Leu Ser			
565	570	575	
Glu Arg Ser Ala Arg Gln Ser Thr Gly Arg Val Gly Val Val Leu Val			
580	585	590	
Val Thr Leu Ser His Asn Ser Arg Arg Ile Asp Val Asp Ile Asn Leu			
595	600	605	
Asp Asn Gln Ala Asp Asp His Arg Leu Arg Val Leu Val Pro Thr Pro			
610	615	620	
Phe Asn Thr Asp Ser Val Leu Ala Asp Thr Gln Phe Gly Ser Leu Thr			
625	630	635	640
Arg Pro Val Asn Asp Ser Ala Met Asn Asn Trp Gln Gln Glu Gly Trp			
645	650	655	
Lys Glu Ala Pro Val Pro Val Trp Asn Met Leu Asn Tyr Val Ala Leu			
660	665	670	
Gln Glu Gly Arg Asn Gly Met Ala Val Phe Ser Glu Gly Leu Arg Glu			
675	680	685	
Phe Glu Val Ile Gly Glu Glu Lys Lys Thr Phe Ala Ile Thr Leu Leu			
690	695	700	
Arg Gly Val Gly Leu Leu Gly Lys Glu Asp Leu Leu Leu Arg Pro Gly			
705	710	715	720
Arg Pro Ser Gly Ile Lys Met Pro Val Pro Asp Ser Gln Leu Arg Gly			
725	730	735	
Leu Leu Ser Cys Arg Leu Ser Leu Leu Ser Tyr Thr Gly Thr Pro Thr			
740	745	750	
Ala Ala Gly Val Ala Gln Gln Ala Arg Ala Trp Leu Thr Pro Val Gln			
755	760	765	
Cys Tyr Asn Lys Ile Pro Trp Asp Val Met Lys Leu Asn Lys Ala Gly			
770	775	780	

Phe	Asn	Val	Pro	Glu	Ser	Tyr	Ser	Leu	Leu	Lys	Met	Pro	Pro	Val	Gly
785				790				795							800
Cys	Leu	Ile	Ser	Ala	Leu	Lys	Lys	Ala	Glu	Asp	Arg	Gln	Glu	Val	Ile
				805				810							815
Leu	Arg	Leu	Phe	Asn	Pro	Ala	Glu	Ser	Ala	Thr	Cys	Asp	Ala	Thr	Val
				820				825							830
Ala	Phe	Ser	Arg	Glu	Val	Ile	Ser	Cys	Ser	Glu	Thr	Met	Met	Asp	Glu
				835				840							845
His	Ile	Thr	Thr	Glu	Glu	Asn	Gln	Gly	Ser	Asn	Leu	Ser	Gly	Pro	Phe
				850				855							860
Leu	Pro	Gly	Gln	Ser	Arg	Thr	Phe	Ser	Tyr	Arg	Leu	Ala			
				865				870							875

<210> 354
<211> 523
<212> PRT
<213> E. Coli

<400> 354															
Met	Met	Leu	Asp	Ile	Val	Glu	Leu	Ser	Arg	Leu	Gln	Phe	Ala	Leu	Thr
1				5				10							15
Ala	Met	Tyr	His	Phe	Leu	Phe	Val	Pro	Leu	Thr	Leu	Gly	Met	Ala	Phe
					20			25							30
Leu	Leu	Ala	Ile	Met	Glu	Thr	Val	Tyr	Val	Leu	Ser	Gly	Lys	Gln	Ile
				35				40							45
Tyr	Lys	Asp	Met	Thr	Lys	Phe	Trp	Gly	Lys	Leu	Phe	Gly	Ile	Asn	Phe
				50			55								60
Ala	Leu	Gly	Val	Ala	Thr	Gly	Leu	Thr	Met	Glu	Phe	Gln	Phe	Gly	Thr
				65			70		75						80
Asn	Trp	Ser	Tyr	Tyr	Ser	His	Tyr	Val	Gly	Asp	Ile	Phe	Gly	Ala	Pro
					85			90							95
Leu	Ala	Ile	Glu	Gly	Leu	Met	Ala	Phe	Phe	Leu	Glu	Ser	Thr	Phe	Val
				100			105								110
Gly	Leu	Phe	Phe	Gly	Trp	Asp	Arg	Leu	Gly	Lys	Val	Gln	His	Met	
				115			120								125
Cys	Val	Thr	Trp	Leu	Val	Ala	Leu	Gly	Ser	Asn	Leu	Ser	Ala	Leu	Trp
				130			135								140
Ile	Leu	Val	Ala	Asn	Gly	Trp	Met	Gln	Asn	Pro	Ile	Ala	Ser	Asp	Phe
				145			150		155						160
Asn	Phe	Glu	Thr	Met	Arg	Met	Glu	Met	Val	Ser	Phe	Ser	Glu	Leu	Val
					165			170							175
Leu	Asn	Pro	Val	Ala	Gln	Val	Lys	Phe	Val	His	Thr	Val	Ala	Ser	Gly
					180		185								190
Tyr	Val	Thr	Gly	Ala	Met	Phe	Ile	Leu	Gly	Ile	Ser	Ala	Trp	Tyr	Met
					195		200								205
Leu	Lys	Gly	Arg	Asp	Phe	Ala	Phe	Ala	Lys	Arg	Ser	Phe	Ala	Ile	Ala
					210		215								220
Ala	Ser	Phe	Gly	Met	Ala	Ala	Val	Leu	Ser	Val	Ile	Val	Leu	Gly	Asp
					225		230		235						240
Glu	Ser	Gly	Tyr	Glu	Met	Gly	Asp	Val	Gln	Lys	Thr	Lys	Leu	Ala	Ala
					245		250								255
Ile	Glu	Ala	Glu	Trp	Glu	Thr	Gln	Pro	Ala	Pro	Ala	Ala	Phe	Thr	Leu
					260		265								270
Phe	Gly	Ile	Pro	Asp	Gln	Glu	Glu	Thr	Asn	Lys	Phe	Ala	Ile	Gln	
					275		280		285						
Ile	Pro	Tyr	Ala	Leu	Gly	Ile	Ile	Ala	Thr	Arg	Ser	Val	Asp	Thr	Pro

290	295	300
Val Ile Gly Leu Lys Glu Leu Met Val Gln His	Glu Glu Arg Ile Arg	
305	310	315
Asn Gly Met Lys Ala Tyr Ser Leu Leu Glu Gln Leu Arg Ser Gly Ser		320
325	330	335
Thr Asp Gln Ala Val Arg Asp Gln Phe Asn Ser Met Lys Lys Asp Leu		
340	345	350
Gly Tyr Gly Leu Leu Leu Lys Arg Tyr Thr Pro Asn Val Ala Asp Ala		
355	360	365
Thr Glu Ala Gln Ile Gln Gln Ala Thr Lys Asp Ser Ile Pro Arg Val		
370	375	380
Ala Pro Leu Tyr Phe Ala Phe Arg Ile Met Val Ala Cys Gly Phe Leu		
385	390	395
Leu Leu Ala Ile Ala Leu Ser Phe Trp Ser Val Ile Arg Asn Arg		400
405	410	415
Ile Gly Glu Lys Lys Trp Leu Leu Arg Ala Ala Leu Tyr Gly Ile Pro		
420	425	430
Leu Pro Trp Ile Ala Val Glu Ala Gly Trp Phe Val Ala Glu Tyr Gly		
435	440	445
Arg Gln Pro Trp Ala Ile Gly Glu Val Leu Pro Thr Ala Val Ala Asn		
450	455	460
Ser Ser Leu Thr Ala Gly Asp Leu Ile Phe Ser Met Val Leu Ile Cys		
465	470	475
Gly Leu Tyr Thr Leu Phe Leu Val Ala Glu Leu Phe Leu Met Phe Lys		
485	490	495
Phe Ala Arg Leu Gly Pro Ser Ser Leu Lys Thr Gly Arg Tyr His Phe		
500	505	510
Glu Gln Ser Ser Thr Thr Gln Pro Ala Arg		
515	520	

<210> 355

<211> 379

<212> PRT

<213> E. Coli

<400> 355

Met Ile Asp Tyr Glu Val Leu Arg Phe Ile Trp Trp Leu Leu Val Gly		
1	5	10
Val Leu Leu Ile Gly Phe Ala Val Thr Asp Gly Phe Asp Met Gly Val		
20	25	30
Gly Met Leu Thr Arg Phe Leu Gly Arg Asn Asp Thr Glu Arg Arg Ile		
35	40	45
Met Ile Asn Ser Ile Ala Pro His Trp Asp Gly Asn Gln Val Trp Leu		
50	55	60
Ile Thr Ala Gly Gly Ala Leu Phe Ala Ala Trp Pro Met Val Tyr Ala		
65	70	75
80		
Ala Ala Phe Ser Gly Phe Tyr Val Ala Met Ile Leu Val Leu Ala Ser		
85	90	95
Leu Phe Phe Arg Pro Val Gly Phe Asp Tyr Arg Ser Lys Ile Glu Glu		
100	105	110
Thr Arg Trp Arg Asn Met Trp Asp Trp Gly Ile Phe Ile Gly Ser Phe		
115	120	125
Val Pro Pro Leu Val Ile Gly Val Ala Phe Gly Asn Leu Leu Gln Gly		
130	135	140
Val Pro Phe Asn Val Asp Glu Tyr Leu Arg Leu Tyr Tyr Thr Gly Asn		
145	150	155
		160

Phe	Phe	Gln	Leu	Leu	Asn	Pro	Phe	Gly	Leu	Leu	Ala	Gly	Val	Val	Ser
							165		170						175
Val	Gly	Met	Ile	Ile	Thr	Gln	Gly	Ala	Thr	Tyr	Leu	Gln	Met	Arg	Thr
							180		185						190
Val	Gly	Glu	Leu	His	Leu	Arg	Thr	Arg	Ala	Thr	Ala	Gln	Val	Ala	Ala
							195		200						205
Leu	Val	Thr	Leu	Val	Cys	Phe	Ala	Leu	Ala	Gly	Val	Trp	Val	Met	Tyr
						210		215				220			
Gly	Ile	Asp	Gly	Tyr	Val	Val	Lys	Ser	Thr	Met	Asp	His	Tyr	Ala	Ala
						225		230			235				240
Ser	Asn	Pro	Leu	Asn	Lys	Glu	Val	Val	Arg	Glu	Ala	Gly	Ala	Trp	Leu
						245				250					255
Val	Asn	Phe	Asn	Asn	Thr	Pro	Ile	Leu	Trp	Ala	Ile	Pro	Ala	Leu	Gly
						260			265						270
Val	Val	Leu	Pro	Leu	Leu	Thr	Ile	Leu	Thr	Ala	Arg	Met	Asp	Lys	Ala
						275		280				285			
Ala	Trp	Ala	Phe	Val	Phe	Ser	Ser	Leu	Thr	Leu	Ala	Cys	Ile	Ile	Leu
						290		295				300			
Thr	Ala	Gly	Ile	Ala	Met	Phe	Pro	Phe	Val	Met	Pro	Ser	Ser	Thr	Met
						305		310			315				320
Met	Asn	Ala	Ser	Leu	Thr	Met	Trp	Asp	Ala	Thr	Ser	Ser	Gln	Leu	Thr
						325			330						335
Leu	Asn	Val	Met	Thr	Trp	Val	Ala	Val	Val	Leu	Val	Pro	Ile	Ile	Leu
						340			345						350
Leu	Tyr	Thr	Ala	Trp	Cys	Tyr	Trp	Lys	Met	Phe	Gly	Arg	Ile	Thr	Lys
						355		360				365			
Glu	Asp	Ile	Glu	Arg	Asn	Thr	His	Ser	Leu	Tyr					
						370		375							

<210> 356
<211> 456
<212> PRT
<213> E. Col

<400> 356

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Met Glu Leu Ser Ser Leu Thr Ala Val Ser Pro Val Asp Gly Arg Tyr
   1           5           10          15
Gly Asp Lys Val Ser Ala Leu Arg Gly Ile Phe Ser Glu Tyr Gly Leu
   20          25          30
Leu Lys Phe Arg Val Gln Val Glu Val Arg Trp Leu Gln Lys Leu Ala
   35          40          45
Ala His Ala Ala Ile Lys Glu Val Pro Ala Phe Ala Ala Asp Ala Ile
   50          55          60
Gly Tyr Leu Asp Ala Ile Val Ala Ser Phe Ser Glu Glu Asp Ala Ala
   65          70          75          80
Arg Ile Lys Thr Ile Glu Arg Thr Thr Asn His Asp Val Lys Ala Val
   85          90          95
Glu Tyr Phe Leu Lys Glu Lys Val Ala Glu Ile Pro Glu Leu His Ala
  100          105         110
Val Ser Glu Phe Ile His Phe Ala Cys Thr Ser Glu Asp Ile Asn Asn
  115          120         125
Leu Ser His Ala Leu Met Leu Lys Thr Ala Arg Asp Glu Val Ile Leu
  130          135         140
Pro Tyr Trp Arg Gln Leu Ile Asp Gly Ile Lys Asp Leu Ala Val Gln
  145          150         155         160
Tyr Arg Asp Ile Pro Leu Leu Ser Arg Thr His Gly Gln Pro Ala Thr

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	165	170	175
Pro Ser Thr Ile Gly Lys Glu Met Ala Asn Val Ala Tyr Arg Met Glu			
180	185	190	
Arg Gln Tyr Arg Gln Leu Asn Gln Val Glu Ile Leu Gly Lys Ile Asn			
195	200	205	
Gly Ala Val Gly Asn Tyr Asn Ala His Ile Ala Ala Tyr Pro Glu Val			
210	215	220	
Asp Trp His Gln Phe Ser Glu Glu Phe Val Thr Ser Leu Gly Ile Gln			
225	230	235	240
Trp Asn Pro Tyr Thr Thr Gln Ile Glu Pro His Asp Tyr Ile Ala Glu			
245	250	255	
Leu Phe Asp Cys Val Ala Arg Phe Asn Thr Ile Leu Ile Asp Phe Asp			
260	265	270	
Arg Asp Val Trp Gly Tyr Ile Ala Leu Asn His Phe Lys Gln Lys Thr			
275	280	285	
Ile Ala Gly Glu Ile Gly Ser Ser Thr Met Pro His Lys Val Asn Pro			
290	295	300	
Ile Asp Phe Glu Asn Ser Glu Gly Asn Leu Gly Leu Ser Asn Ala Val			
305	310	315	320
Leu Gln His Leu Ala Ser Lys Leu Pro Val Ser Arg Trp Gln Arg Asp			
325	330	335	
Leu Thr Asp Ser Thr Val Leu Arg Asn Leu Gly Val Gly Ile Gly Tyr			
340	345	350	
Ala Leu Ile Ala Tyr Gln Ser Thr Leu Lys Gly Val Ser Lys Leu Glu			
355	360	365	
Val Asn Arg Asp His Leu Leu Asp Glu Leu Asp His Asn Trp Glu Val			
370	375	380	
Leu Ala Glu Pro Ile Gln Thr Val Met Arg Arg Tyr Gly Ile Glu Lys			
385	390	395	400
Pro Tyr Glu Lys Leu Lys Glu Leu Thr Arg Gly Lys Arg Val Asp Ala			
405	410	415	
Glu Gly Met Lys Gln Phe Ile Asp Gly Leu Ala Leu Pro Glu Glu Glu			
420	425	430	
Lys Ala Arg Leu Lys Ala Met Thr Pro Ala Asn Tyr Ile Gly Arg Ala			
435	440	445	
Ile Thr Met Val Asp Glu Leu Lys			
450	455		

<210> 357

<211> 61

<212> PRT

<213> E. Coli

<400> 357

Met Leu Ile Leu Thr Arg Arg Val Gly Glu Thr Leu Met Ile Gly Asp			
1	5	10	15
Glu Val Thr Val Thr Val Leu Gly Val Lys Gly Asn Gln Val Arg Ile			
20	25	30	
Gly Val Asn Ala Pro Lys Glu Val Ser Val His Arg Glu Glu Ile Tyr			
35	40	45	
Gln Arg Ile Gln Ala Glu Lys Ser Gln Gln Ser Ser Tyr			
50	55	60	

<210> 358

<211> 93

<212> RNA

<213> E. Coli

<400> 358

ggugaggugg ccgagaggcu gaaggcguc cccugcuaag ggaguauugcg gucaaaagcu
gcauccgggg uucgaauccc cgccucaccc cca

60

93

<210> 359

<211> 200

<212> PRT

<213> E. Coli

<400> 359

Met Lys Asn Lys Ala Asp Asn Lys Lys Arg Asn Phe Leu Thr His Ser
1 5 10 15
Glu Ile Glu Ser Leu Leu Lys Ala Ala Asn Thr Gly Pro His Ala Ala
20 25 30
Arg Asn Tyr Cys Leu Thr Leu Leu Cys Phe Ile His Gly Phe Arg Ala
35 40 45
Ser Glu Ile Cys Arg Leu Arg Ile Ser Asp Ile Asp Leu Lys Ala Lys
50 55 60
Cys Ile Tyr Ile His Arg Leu Lys Lys Gly Phe Ser Thr Thr His Pro
65 70 75 80
Leu Leu Asn Lys Glu Val Gln Ala Leu Lys Asn Trp Leu Ser Ile Arg
85 90 95
Thr Ser Tyr Pro His Ala Glu Ser Glu Trp Val Phe Leu Ser Arg Lys
100 105 110
Gly Asn Pro Leu Ser Arg Gln Gln Phe Tyr His Ile Ile Ser Thr Ser
115 120 125
Gly Gly Asn Ala Gly Leu Ser Leu Glu Ile His Pro His Met Leu Arg
130 135 140
His Ser Cys Gly Phe Ala Leu Ala Asn Met Gly Ile Asp Thr Arg Leu
145 150 155 160
Ile Gln Asp Tyr Leu Gly His Arg Asn Ile Arg His Thr Val Trp Tyr
165 170 175
Thr Ala Ser Asn Ala Gly Arg Phe Tyr Gly Ile Trp Asp Arg Ala Arg
180 185 190
Gly Arg Gln Arg His Ala Val Leu
195 200

<210> 360

<211> 198

<212> PRT

<213> E. Coli

<400> 360

Met Ser Lys Arg Arg Tyr Leu Thr Gly Lys Glu Val Gln Ala Met Met
1 5 10 15
Gln Ala Val Cys Tyr Gly Ala Thr Gly Ala Arg Asp Tyr Cys Leu Ile
20 25 30
Leu Leu Ala Tyr Arg His Gly Met Arg Ile Ser Glu Leu Leu Asp Leu
35 40 45
His Tyr Gln Asp Leu Asp Leu Asn Glu Gly Arg Ile Asn Ile Arg Arg
50 55 60
Leu Lys Asn Gly Phe Ser Thr Val His Pro Leu Arg Phe Asp Glu Arg

65	70	75	80
Glu Ala Val Glu Arg Trp Thr Gln Glu Arg Ala Asn Trp Lys Gly Ala			
85	90	95	
Asp Arg Thr Asp Ala Ile Phe Ile Ser Arg Arg Gly Ser Arg Leu Ser			
100	105	110	
Arg Gln Gln Ala Tyr Arg Ile Ile Arg Asp Ala Gly Ile Glu Ala Gly			
115	120	125	
Thr Val Thr Gln Thr His Pro His Met Leu Arg His Ala Cys Gly Tyr			
130	135	140	
Glu Leu Ala Glu Arg Gly Ala Asp Thr Arg Leu Ile Gln Asp Tyr Leu			
145	150	155	160
Gly His Arg Asn Ile Arg His Thr Val Arg Tyr Thr Ala Ser Asn Ala			
165	170	175	
Ala Arg Phe Ala Gly Leu Trp Glu Arg Asn Asn Leu Ile Asn Glu Lys			
180	185	190	
Leu Lys Arg Glu Glu Val			
195			

<210> 361

<211> 182

<212> PRT

<213> E. Coli

<400> 361

Met Lys Ile Lys Thr Leu Ala Ile Val Val Leu Ser Ala Leu Ser Leu			
1	5	10	15
Ser Ser Thr Ala Ala Leu Ala Ala Ala Thr Thr Val Asn Gly Gly Thr			
20	25	30	
Val His Phe Lys Gly Glu Val Val Asn Ala Ala Cys Ala Val Asp Ala			
35	40	45	
Gly Ser Val Asp Gln Thr Val Gln Leu Gly Gln Val Arg Thr Ala Ser			
50	55	60	
Leu Ala Gln Glu Gly Ala Thr Ser Ser Ala Val Gly Phe Asn Ile Gln			
65	70	75	80
Leu Asn Asp Cys Asp Thr Asn Val Ala Ser Lys Ala Ala Val Ala Phe			
85	90	95	
Leu Gly Thr Ala Ile Asp Ala Gly His Thr Asn Val Leu Ala Leu Gln			
100	105	110	
Ser Ser Ala Ala Gly Ser Ala Thr Asn Val Gly Val Gln Ile Leu Asp			
115	120	125	
Arg Thr Gly Ala Ala Leu Thr Leu Asp Gly Ala Thr Phe Ser Ser Glu			
130	135	140	
Thr Thr Leu Asn Asn Gly Thr Asn Thr Ile Pro Phe Gln Ala Arg Tyr			
145	150	155	160
Phe Ala Thr Gly Ala Ala Thr Pro Gly Ala Ala Asn Ala Asp Ala Thr			
165	170	175	
Phe Lys Val Gln Tyr Gln			
180			

<210> 362

<211> 215

<212> PRT

<213> E. Coli

<400> 362

Met Leu Leu Met Arg Met Arg Pro Ser Arg Phe Ser Ile Asn Asn Leu
1 5 10 15
Pro Arg Phe Arg Asp Val Ile Thr Gly Arg Asp Ala His Pro Cys Ala
20 25 30
Ile Lys Ile Thr Met Lys Arg Lys Arg Leu Phe Leu Leu Ala Ser Leu
35 40 45
Leu Pro Met Phe Ala Leu Ala Gly Asn Lys Trp Asn Thr Thr Leu Pro
50 55 60
Gly Gly Asn Met Gln Phe Gln Gly Val Ile Ile Ala Glu Thr Cys Arg
65 70 75 80
Ile Glu Ala Gly Asp Lys Gln Met Thr Val Asn Met Gly Gln Ile Ser
85 90 95
Ser Asn Arg Phe His Ala Val Gly Glu Asp Ser Ala Pro Val Pro Phe
100 105 110
Val Ile His Leu Arg Glu Cys Ser Thr Val Val Ser Glu Arg Val Gly
115 120 125
Val Ala Phe His Gly Val Ala Asp Gly Lys Asn Pro Asp Val Leu Ser
130 135 140
Val Gly Glu Gly Pro Gly Ile Ala Thr Asn Ile Gly Val Ala Leu Phe
145 150 155 160
Asp Asp Glu Gly Asn Leu Val Pro Ile Asn Arg Pro Pro Ala Asn Trp
165 170 175
Lys Arg Leu Tyr Ser Gly Ser Thr Ser Leu His Phe Ile Ala Lys Tyr
180 185 190
Arg Ala Thr Gly Arg Arg Val Thr Gly Gly Ile Ala Asn Ala Gln Ala
195 200 205
Trp Phe Ser Leu Thr Tyr Gln
210 215

<210> 363

<211> 241

<212> PRT

<213> E. Coli

<400> 363

Met Ser Asn Lys Asn Val Asn Val Arg Lys Ser Gln Glu Ile Thr Phe
1 5 10 15
Cys Leu Leu Ala Gly Ile Leu Met Phe Met Ala Met Met Val Ala Gly
20 25 30
Arg Ala Glu Ala Gly Val Ala Leu Gly Ala Thr Arg Val Ile Tyr Pro
35 40 45
Ala Gly Gln Lys Gln Glu Gln Leu Ala Val Thr Asn Asn Asp Glu Asn
50 55 60
Ser Thr Tyr Leu Ile Gln Ser Trp Val Glu Asn Ala Asp Gly Val Lys
65 70 75 80
Asp Gly Arg Phe Ile Val Thr Pro Pro Leu Phe Ala Met Lys Gly Lys
85 90 95
Lys Glu Asn Thr Leu Arg Ile Leu Asp Ala Thr Asn Asn Gln Leu Pro
100 105 110
Gln Asp Arg Glu Ser Leu Phe Trp Met Asn Val Lys Ala Ile Pro Ser
115 120 125
Met Asp Lys Ser Lys Leu Thr Glu Asn Thr Leu Gln Leu Ala Ile Ile
130 135 140
Ser Arg Ile Lys Leu Tyr Tyr Arg Pro Ala Lys Leu Ala Leu Pro Pro

145	150	155	160
Asp Gln Ala Ala Glu Lys Leu Arg Phe Arg Arg Ser Ala Asn Ser Leu			
165	170	175	
Thr Leu Ile Asn Pro Thr Pro Tyr Tyr Leu Thr Val Thr Glu Leu Asn			
180	185	190	
Ala Gly Thr Arg Val Leu Glu Asn Ala Leu Val Pro Pro Met Gly Glu			
195	200	205	
Ser Thr Val Lys Leu Pro Ser Asp Ala Gly Ser Asn Ile Thr Tyr Arg			
210	215	220	
Thr Ile Asn Asp Tyr Gly Ala Leu Thr Pro Lys Met Thr Gly Val Met			
225	230	235	240
Glu			

<210> 364
 <211> 878
 <212> PRT
 <213> E. Coli

<400> 364

Met Ser Tyr Leu Asn Leu Arg Leu Tyr Gln Arg Asn Thr Gln Cys Leu			
1	5	10	15
His Ile Arg Lys His Arg Leu Ala Gly Phe Phe Val Arg Leu Val Val			
20	25	30	
Ala Cys Ala Phe Ala Ala Gln Ala Pro Leu Ser Ser Ala Asp Leu Tyr			
35	40	45	
Phe Asn Pro Arg Phe Leu Ala Asp Asp Pro Gln Ala Val Ala Asp Leu			
50	55	60	
Ser Arg Phe Glu Asn Gly Gln Glu Leu Pro Pro Gly Thr Tyr Arg Val			
65	70	75	80
Asp Ile Tyr Leu Asn Asn Gly Tyr Met Ala Thr Arg Asp Val Thr Phe			
85	90	95	
Asn Thr Gly Asp Ser Glu Gln Gly Ile Val Pro Cys Leu Thr Arg Ala			
100	105	110	
Gln Leu Ala Ser Met Gly Leu Asn Thr Ala Ser Val Ala Gly Met Asn			
115	120	125	
Leu Leu Ala Asp Asp Ala Cys Val Pro Leu Thr Thr Met Val Gln Asp			
130	135	140	
Ala Thr Ala His Leu Asp Val Gly Gln Gln Arg Leu Asn Leu Thr Ile			
145	150	155	160
Pro Gln Ala Phe Met Ser Asn Arg Ala Arg Gly Tyr Ile Pro Pro Glu			
165	170	175	
Leu Trp Asp Pro Gly Ile Asn Ala Gly Leu Leu Asn Tyr Asn Phe Ser			
180	185	190	
Gly Asn Ser Val Gln Asn Arg Ile Gly Gly Asn Ser His Tyr Ala Tyr			
195	200	205	
Leu Asn Leu Gln Ser Gly Leu Asn Ile Gly Ala Trp Arg Leu Arg Asp			
210	215	220	
Asn Thr Thr Trp Ser Tyr Asn Ser Ser Asp Arg Ser Ser Gly Ser Lys			
225	230	235	240
Asn Lys Trp Gln His Ile Asn Thr Trp Leu Glu Arg Asp Ile Ile Pro			
245	250	255	
Leu Arg Ser Arg Leu Thr Leu Gly Asp Gly Tyr Thr Gln Gly Asp Ile			
260	265	270	
Phe Asp Gly Ile Asn Phe Arg Gly Ala Gln Leu Ala Ser Asp Asp Asn			
275	280	285	

Met Leu Pro Asp Ser Gln Arg Gly Phe Ala Pro Val Ile His Gly Ile
 290 295 300
 Ala Arg Gly Thr Ala Gln Val Thr Ile Lys Gln Asn Gly Tyr Asp Ile
 305 310 315 320
 Tyr Asn Ser Thr Val Pro Pro Gly Pro Phe Thr Ile Asn Asp Ile Tyr
 325 330 335
 Ala Ala Gly Asn Ser Gly Asp Leu Gln Val Thr Ile Lys Glu Ala Asp
 340 345 350
 Gly Ser Thr Gln Ile Phe Thr Val Pro Tyr Ser Ser Val Pro Leu Leu
 355 360 365
 Gln Arg Glu Gly His Thr Arg Tyr Ser Ile Thr Ala Gly Glu Tyr Arg
 370 375 380
 Ser Gly Asn Ala Gln Gln Glu Lys Thr Arg Phe Phe Gln Ser Thr Leu
 385 390 395 400
 Leu His Gly Leu Pro Ala Gly Trp Thr Ile Tyr Gly Gly Thr Gln Leu
 405 410 415
 Ala Asp Arg Tyr Arg Ala Phe Asn Phe Gly Ile Gly Lys Asn Met Gly
 420 425 430
 Ala Leu Gly Ala Leu Ser Val Asp Met Thr Gln Ala Asn Ser Thr Leu
 435 440 445
 Pro Asp Asp Ser Gln His Asp Gly Gln Ser Val Arg Phe Leu Tyr Asn
 450 455 460
 Lys Ser Leu Asn Glu Ser Gly Thr Asn Ile Gln Leu Val Gly Tyr Arg
 465 470 475 480
 Tyr Ser Thr Ser Gly Tyr Phe Asn Phe Ala Asp Thr Thr Tyr Ser Arg
 485 490 495
 Met Asn Gly Tyr Asn Ile Glu Thr Gln Asp Gly Val Ile Gln Val Lys
 500 505 510
 Pro Lys Phe Thr Asp Tyr Tyr Asn Leu Ala Tyr Asn Lys Arg Gly Lys
 515 520 525
 Leu Gln Leu Thr Val Thr Gln Gln Leu Gly Arg Thr Ser Thr Leu Tyr
 530 535 540
 Leu Ser Gly Ser His Gln Thr Tyr Trp Gly Thr Ser Asn Val Asp Glu
 545 550 555 560
 Gln Phe Gln Ala Gly Leu Asn Thr Ala Phe Glu Asp Ile Asn Trp Thr
 565 570 575
 Leu Ser Tyr Ser Leu Thr Lys Asn Ala Trp Gln Lys Gly Arg Asp Gln
 580 585 590
 Met Leu Ala Leu Asn Val Asn Ile Pro Phe Ser His Trp Leu Arg Ser
 595 600 605
 Asp Ser Lys Ser Gln Trp Arg His Ala Ser Ala Ser Tyr Ser Met Ser
 610 615 620
 His Asp Leu Asn Gly Arg Met Thr Asn Leu Ala Gly Val Tyr Gly Thr
 625 630 635 640
 Leu Leu Glu Asp Asn Asn Leu Ser Tyr Ser Val Gln Thr Gly Tyr Ala
 645 650 655
 Gly Gly Gly Asp Gly Asn Ser Gly Ser Thr Gly Tyr Ala Thr Leu Asn
 660 665 670
 Tyr Arg Gly Gly Tyr Gly Asn Ala Asn Ile Gly Tyr Ser His Ser Asp
 675 680 685
 Asp Ile Lys Gln Leu Tyr Tyr Gly Val Ser Gly Gly Val Leu Ala His
 690 695 700
 Ala Asn Gly Val Thr Leu Gly Gln Pro Leu Asn Asp Thr Val Val Leu
 705 710 715 720
 Val Lys Ala Pro Gly Ala Lys Asp Ala Lys Val Glu Asn Gln Thr Gly
 725 730 735
 Val Arg Thr Asp Trp Arg Gly Tyr Ala Val Leu Pro Tyr Ala Thr Glu

740	745	750	
Tyr Arg Glu Asn Arg Val Ala Leu Asp Thr Asn Thr	Leu Ala Asp Asn		
755	760	765	
Val Asp Leu Asp Asn Ala Val Ala Asn Val Val Pro	Thr Arg Gly Ala		
770	775	780	
Ile Val Arg Ala Glu Phe Lys Ala Arg Val Gly Ile	Lys Leu Leu Met		
785	790	795	800
Thr Leu Thr His Asn Asn Lys Pro Leu Pro Phe Gly	Ala Met Val Thr		
805	810	815	
Ser Glu Ser Ser Gln Ser Ser Gly Ile Val Ala Asp	Asn Gly Gln Val		
820	825	830	
Tyr Leu Ser Gly Met Pro Leu Ala Gly Lys Val Gln	Val Lys Trp Gly		
835	840	845	
Glu Glu Glu Asn Ala His Cys Val Ala Asn Tyr Gln	Leu Pro Pro Glu		
850	855	860	
Ser Gln Gln Gln Leu Leu Thr Gln Leu Ser Ala Glu	Cys Arg		
865	870	875	

<210> 365

<211> 176

<212> PRT

<213> E. Coli

<400> 365

Met Arg Asn Lys Pro Phe Tyr Leu Leu Cys Ala Phe	Leu Trp Leu Ala		
1	5	10	15
Val Ser His Ala Leu Ala Ala Asp Ser Thr Ile	Thr Ile Arg Gly Tyr		
20	25	30	
Val Arg Asp Asn Gly Cys Ser Val Ala Ala Glu	Ser Thr Asn Phe Thr		
35	40	45	
Val Asp Leu Met Glu Asn Ala Ala Lys Gln Phe	Asn Asn Ile Gly Ala		
50	55	60	
Thr Thr Pro Val Val Pro Phe Arg Ile Leu Leu	Ser Pro Cys Gly Asn		
65	70	75	80
Ala Val Ser Ala Val Lys Val Gly Phe Thr Gly	Val Ala Asp Ser His		
85	90	95	
Asn Ala Asn Leu Leu Ala Leu Glu Asn Thr Val	Ser Ala Ala Ser Gly		
100	105	110	
Leu Gly Ile Gln Leu Leu Asn Glu Gln Gln Asn	Gln Ile Pro Leu Asn		
115	120	125	
Ala Pro Ser Ser Ala Leu Ser Trp Thr Thr Leu	Thr Pro Gly Lys Pro		
130	135	140	
Asn Thr Leu Asn Phe Tyr Ala Arg Leu Met Ala	Thr Gln Val Pro Val		
145	150	155	160
Thr Ala Gly His Ile Asn Ala Thr Ala Thr Phe	Thr Leu Glu Tyr Gln		
165	170	175	

<210> 366

<211> 167

<212> PRT

<213> E. Coli

<400> 366

Met Lys Trp Cys Lys Arg Gly Tyr Val Leu Ala Ala Ile Leu Ala Leu

1	5	10	15
Ala Ser Ala Thr Ile Gln Ala Ala Asp Val Thr Ile Thr Val Asn Gly			
20	25	30	
Lys Val Val Ala Lys Pro Cys Thr Val Ser Thr Thr Asn Ala Thr Val			
35	40	45	
Asp Leu Gly Asp Leu Tyr Ser Phe Ser Leu Met Ser Ala Gly Ala Ala			
50	55	60	
Ser Ala Trp His Asp Val Ala Leu Glu Leu Thr Asn Cys Pro Val Gly			
65	70	75	80
Thr Ser Arg Val Thr Ala Ser Phe Ser Gly Ala Ala Asp Ser Thr Gly			
85	90	95	
Tyr Tyr Lys Asn Gln Gly Thr Ala Gln Asn Ile Gln Leu Glu Leu Gln			
100	105	110	
Asp Asp Ser Gly Asn Thr Leu Asn Thr Gly Ala Thr Lys Thr Val Gln			
115	120	125	
Val Asp Asp Ser Ser Gln Ser Ala His Phe Pro Leu Gln Val Arg Ala			
130	135	140	
Leu Thr Val Asn Gly Gly Ala Thr Gln Gly Thr Ile Gln Ala Val Ile			
145	150	155	160
Ser Ile Thr Tyr Thr Tyr Ser			
165			

<210> 367
 <211> 300
 <212> PRT
 <213> E. Coli

<400> 367			
Met Lys Arg Val Ile Thr Leu Phe Ala Val Leu Leu Met Gly Trp Ser			
1	5	10	15
Val Asn Ala Trp Ser Phe Ala Cys Lys Thr Ala Asn Gly Thr Ala Ile			
20	25	30	
Pro Ile Gly Gly Ser Ala Asn Val Tyr Val Asn Leu Ala Pro Val			
35	40	45	
Val Asn Val Gly Gln Asn Leu Val Val Asp Leu Ser Thr Gln Ile Phe			
50	55	60	
Cys His Asn Asp Tyr Pro Glu Thr Ile Thr Asp Tyr Val Thr Leu Gln			
65	70	75	80
Arg Gly Ser Ala Tyr Gly Gly Val Leu Ser Asn Phe Ser Gly Thr Val			
85	90	95	
Lys Tyr Ser Gly Ser Ser Tyr Pro Phe Pro Thr Thr Ser Glu Thr Pro			
100	105	110	
Arg Val Val Tyr Asn Ser Arg Thr Asp Lys Pro Trp Pro Val Ala Leu			
115	120	125	
Tyr Leu Thr Pro Val Ser Ser Ala Gly Gly Val Ala Ile Lys Ala Gly			
130	135	140	
Ser Leu Ile Ala Val Leu Ile Leu Arg Gln Thr Asn Asn Tyr Asn Ser			
145	150	155	160
Asp Asp Phe Gln Phe Val Trp Asn Ile Tyr Ala Asn Asn Asp Val Val			
165	170	175	
Val Pro Thr Gly Gly Cys Asp Val Ser Ala Arg Asp Val Thr Val Thr			
180	185	190	
Leu Pro Asp Tyr Pro Gly Ser Val Pro Ile Pro Leu Thr Val Tyr Cys			
195	200	205	
Ala Lys Ser Gln Asn Leu Gly Tyr Tyr Leu Ser Gly Thr Thr Ala Asp			

210	215	220
Ala Gly Asn Ser Ile Phe Thr Asn Thr Ala Ser Phe Ser Pro Ala Gln		
225	230	235
Gly Val Gly Val Gln Leu Thr Arg Asn Gly Thr Ile Ile Pro Ala Asn		
245	250	255
Asn Thr Val Ser Leu Gly Ala Val Gly Thr Ser Ala Val Ser Leu Gly		
260	265	270
Leu Thr Ala Asn Tyr Ala Arg Thr Gly Gly Gln Val Thr Ala Gly Asn		
275	280	285
Val Gln Ser Ile Ile Gly Val Thr Phe Val Tyr Gln		
290	295	300

<210> 368
<211> 521
<212> PRT
<213> E. Coli

<400> 368		
Met Leu Ser Lys Leu Pro Arg Arg Leu Arg Ser Phe Gln Thr Tyr Cys		
1	5	10
Thr Ile Arg Val His Arg Gly Glu Asp Met Lys Ser Met Asp Lys Leu		
20	25	30
Thr Thr Gly Val Ala Tyr Gly Thr Ser Ala Gly Asn Ala Gly Phe Trp		
35	40	45
Ala Leu Gln Leu Leu Asp Lys Val Thr Pro Ser Gln Trp Ala Ala Ile		
50	55	60
Gly Val Leu Gly Ser Leu Val Phe Gly Leu Leu Thr Tyr Leu Thr Asn		
65	70	75
Leu Tyr Phe Lys Ile Lys Glu Asp Arg Arg Lys Ala Ala Arg Gly Glu		
85	90	95
Ser Asn Asp Ser Arg Leu Thr Gly Cys Glu Arg Ser Pro Phe Glu Ser		
100	105	110
Tyr Gly Asn Cys Ser Leu Thr Gly Gln Arg Thr Leu Arg Asn Phe Pro		
115	120	125
Gly Cys Arg His Gly Pro Cys Arg Ser Cys Ala Gly Val Leu Gly Ser		
130	135	140
Ser Gln Lys Glu Arg Pro Ala Ser Leu Pro Gly Ser Ser Arg Lys Ile		
145	150	155
Val Arg Lys Ser Val Leu Ser Ala Ala Ser Val Leu Leu Asp Lys Ser		
165	170	175
Cys Gln Ala Arg Ala Ser Ser Ser Ile Ser Met Asn Thr Lys Ile Arg		
180	185	190
Tyr Gly Leu Ser Ala Ala Val Leu Ala Leu Ile Gly Ala Gly Ala Ser		
195	200	205
Ala Pro Gln Ile Leu Asp Gln Phe Leu Asp Glu Lys Glu Gly Asn His		
210	215	220
Thr Met Ala Tyr Arg Asp Gly Ser Gly Ile Trp Thr Ile Cys Arg Gly		
225	230	235
Ala Thr Val Val Asp Gly Lys Thr Val Phe Pro Asn Met Lys Leu Ser		
245	250	255
Lys Glu Lys Cys Asp Gln Val Asn Ala Ile Glu Arg Asp Lys Ala Leu		
260	265	270
Ala Trp Val Glu Arg Asn Ile Lys Val Pro Leu Thr Glu Pro Gln Lys		
275	280	285
Ala Gly Ile Ala Ser Phe Cys Pro Tyr Asn Ile Gly Pro Gly Lys Cys		

290	295	300
Phe Pro Ser Thr Phe Tyr Lys Arg Leu Asn Ala Gly Asp Arg Lys Gly		
305	310	315
Ala Cys Glu Ala Ile Arg Trp Trp Ile Lys Asp Gly Gly Arg Asp Cys		320
325	330	335
Arg Ile Arg Ser Asn Asn Cys Tyr Gly Gln Val Ile Arg Arg Asp Gln		
340	345	350
Glu Ser Ala Leu Thr Cys Trp Gly Ile Glu Gln Ile Arg Tyr Ser Trp		
355	360	365
Phe Phe Ser Cys Cys Gln Asp Leu Ser Ser Glu Met Ser Gly Ala Thr		
370	375	380
Glu Asp Gly Lys Lys Asn Gly Arg Asn Val Met Leu Pro His Tyr His		
385	390	395
Lys Arg Met Leu Asn Leu Leu Glu Leu Asn Arg Gly Glu Leu Pro		400
405	410	415
Val Met Arg Leu Leu Lys Met Arg Asn Arg Asn Leu Leu Lys Phe Leu		
420	425	430
Pro Gly Leu Leu Ile Cys Leu Ile Val Leu Thr Ser Cys Val Pro Lys		
435	440	445
Gln Lys Asn Met Pro Tyr Ala Leu Thr Gln Arg Ser Ile Pro Gln Ile		
450	455	460
Leu Pro Leu Pro Ser Glu Ala Lys Gln Pro Lys Pro Pro Lys Glu Cys		
465	470	475
Ser Pro Thr Cys Ser Glu Ile Leu Gln Gln Lys Leu Ser Phe Met Leu		
485	490	495
Lys Leu Leu Thr Asn Ala Thr Ser Gln Glu Leu Val Asn Arg Ser Met		
500	505	510
Asn Leu Glu Ile Lys Ser Ile Lys Cys		
515	520	

<210> 369
 <211> 177
 <212> PRT
 <213> E. Coli

<400> 369

Met Asn Thr Lys Ile Arg Tyr Gly Leu Ser Ala Ala Val Leu Ala Leu		
1	5	10
Ile Gly Ala Gly Ala Ser Ala Pro Gln Ile Leu Asp Gln Phe Leu Asp		15
20	25	30
Glu Lys Glu Gly Asn His Thr Met Ala Tyr Arg Asp Gly Ser Gly Ile		
35	40	45
Trp Thr Ile Cys Arg Gly Ala Thr Val Val Asp Gly Lys Thr Val Phe		
50	55	60
Pro Asn Met Lys Leu Ser Lys Glu Lys Cys Asp Gln Val Asn Ala Ile		
65	70	75
Glu Arg Asp Lys Ala Leu Ala Trp Val Glu Arg Asn Ile Lys Val Pro		80
85	90	95
Leu Thr Glu Pro Gln Lys Ala Gly Ile Ala Ser Phe Cys Pro Tyr Asn		
100	105	110
Ile Gly Pro Gly Lys Cys Phe Pro Ser Thr Phe Tyr Lys Arg Leu Asn		
115	120	125
Ala Gly Asp Arg Lys Gly Ala Cys Glu Ala Ile Arg Trp Trp Ile Lys		
130	135	140
Asp Gly Gly Arg Asp Cys Arg Ile Arg Ser Asn Asn Cys Tyr Gly Gln		

145 150 155 160
Val Ile Arg Arg Asp Gln Glu Ser Ala Leu Thr Cys Trp Gly Ile Glu
 165 170 175
Gln

<210> 370
<211> 103
<212> PRT
<213> E. Coli

<400> 370
Met Thr Gln Asp Tyr Glu Leu Val Val Lys Gly Val Arg Asn Phe Glu
1 5 10 15
Asn Lys Val Thr Val Thr Val Ala Leu Gln Asp Lys Glu Arg Phe Asp
20 25 30
Gly Glu Ile Phe Asp Leu Asp Val Ala Met Asp Arg Val Glu Gly Ala
35 40 45
Ala Leu Glu Phe Tyr Glu Ala Ala Ala Arg Arg Ser Val Arg Gln Val
50 55 60
Phe Leu Glu Val Ala Glu Lys Leu Ser Glu Lys Val Glu Ser Tyr Leu
65 70 75 80
Gln His Gln Tyr Ser Phe Lys Ile Glu Asn Pro Ala Asn Lys His Glu
85 90 95
Arg Pro His His Lys Tyr Leu
100

<210> 371
<211> 96
<212> PRT
<213> E. Coli

<400> 371
Met Leu Ser Lys Leu Pro Arg Arg Leu Arg Ser Phe Gln Thr Tyr Cys
1 5 10 15
Thr Ile Arg Val His Arg Gly Glu Asp Met Lys Ser Met Asp Lys Leu
20 25 30
Thr Thr Gly Val Ala Tyr Gly Thr Ser Ala Gly Asn Ala Gly Phe Trp
35 40 45
Ala Leu Gln Leu Leu Asp Lys Val Thr Pro Ser Gln Trp Ala Ala Ile
50 55 60
Gly Val Leu Gly Ser Leu Val Phe Gly Leu Leu Thr Tyr Leu Thr Asn
65 70 75 80
Leu Tyr Phe Lys Ile Lys Glu Asp Arg Arg Lys Ala Ala Arg Gly Glu
85 90 95

<210> 372
<211> 71
<212> PRT
<213> E. Coli

<400> 372

Met Ser Asn Lys Met Thr Gly Leu Val Lys Trp Phe Asn Ala Asp Lys
 1 5 10 15
 Gly Phe Gly Phe Ile Ser Pro Val Asp Gly Ser Lys Asp Val Phe Val
 20 25 30
 His Phe Ser Ala Ile Gln Asn Asp Asn Tyr Arg Thr Leu Phe Glu Gly
 35 40 45
 Gln Lys Val Thr Phe Ser Ile Glu Ser Gly Ala Lys Gly Pro Ala Ala
 50 55 60
 Ala Asn Val Ile Ile Thr Asp
 65 70

<210> 373
 <211> 338
 <212> PRT
 <213> E. Coli

<400> 373
 Met Phe Val Ile Trp Ser His Arg Thr Gly Phe Ile Met Ser His Gln
 1 5 10 15
 Leu Thr Phe Ala Asp Ser Glu Phe Ser Ser Lys Arg Arg Gln Thr Arg
 20 25 30
 Lys Glu Ile Phe Leu Ser Arg Met Glu Gln Ile Leu Pro Trp Gln Asn
 35 40 45
 Met Val Glu Val Ile Glu Pro Phe Tyr Pro Lys Ala Gly Asn Gly Arg
 50 55 60
 Arg Pro Tyr Pro Leu Glu Thr Met Leu Arg Ile His Cys Met Gln His
 65 70 75 80
 Trp Tyr Asn Leu Ser Asp Gly Ala Met Glu Asp Ala Leu Tyr Glu Ile
 85 90 95
 Ala Ser Met Arg Leu Phe Ala Arg Leu Ser Leu Asp Ser Ala Leu Pro
 100 105 110
 Asp Arg Thr Thr Ile Met Asn Phe Arg His Leu Leu Glu Gln His Gln
 115 120 125
 Leu Ala Arg Gln Leu Phe Lys Thr Ile Asn Arg Trp Leu Ala Glu Ala
 130 135 140
 Gly Val Met Met Thr Gln Gly Thr Leu Val Asp Ala Thr Ile Ile Glu
 145 150 155 160
 Ala Pro Ser Ser Thr Lys Asn Lys Glu Gln Gln Arg Asp Pro Glu Met
 165 170 175
 His Gln Thr Lys Lys Gly Asn Gln Trp His Phe Gly Met Lys Ala His
 180 185 190
 Ile Gly Val Asp Ala Lys Ser Gly Leu Thr His Ser Leu Val Thr Thr
 195 200 205
 Ala Ala Asn Glu His Asp Leu Asn Gln Leu Gly Asn Leu Leu His Gly
 210 215 220
 Glu Glu Gln Phe Val Ser Ala Asp Ala Gly Tyr Gln Gly Ala Pro Gln
 225 230 235 240
 Arg Glu Glu Leu Ala Glu Val Asp Val Asp Trp Leu Ile Ala Glu Arg
 245 250 255
 Pro Gly Lys Val Arg Thr Leu Lys Gln His Pro Arg Lys Asn Lys Thr
 260 265 270
 Ala Ile Asn Ile Glu Tyr Met Lys Ala Ser Ile Arg Ala Arg Val Glu
 275 280 285
 His Pro Phe Arg Ile Ile Lys Arg Gln Phe Gly Phe Val Lys Ala Arg
 290 295 300

Tyr Lys Gly Leu Leu Lys Asn Asp Asn Gln Leu Ala Met Leu Phe Thr
 305 310 315 320
 Leu Ala Asn Leu Phe Arg Ala Asp Gln Met Ile Arg Gln Trp Glu Arg
 325 330 335
 Ser His

<210> 374
 <211> 157
 <212> PRT
 <213> E. Coli

<400> 374

Met Val Tyr Ile Ile Val Ser His Gly His Glu Asp Tyr Ile Lys
 1 5 10 15
 Lys Leu Leu Glu Asn Leu Asn Ala Asp Asp Glu His Tyr Lys Ile Ile
 20 25 30
 Val Arg Asp Asn Lys Asp Ser Leu Leu Leu Lys Gln Ile Cys Gln His
 35 40 45
 Tyr Ala Gly Leu Asp Tyr Ile Ser Gly Gly Val Tyr Gly Phe Gly His
 50 55 60
 Asn Asn Asn Ile Ala Val Ala Tyr Val Lys Glu Lys Tyr Arg Pro Ala
 65 70 75 80
 Asp Asp Asp Tyr Ile Leu Phe Leu Asn Pro Asp Ile Ile Met Lys His
 85 90 95
 Asp Asp Leu Leu Thr Tyr Ile Lys Tyr Val Glu Ser Lys Arg Tyr Ala
 100 105 110
 Phe Ser Thr Leu Cys Leu Phe Arg Asp Glu Ala Lys Ser Leu His Asp
 115 120 125
 Tyr Ser Val Arg Lys Phe Pro Val Leu Ser Asp Phe Ile Val Ser Phe
 130 135 140
 Met Leu Gly Ile Lys Glu Gly Ala Asn Lys Ser Leu Ile
 145 150 155

<210> 375
 <211> 372
 <212> PRT
 <213> E. Coli

<400> 375

Met Gly Lys Ser Ile Val Val Val Ser Ala Val Asn Phe Thr Thr Gly
 1 5 10 15
 Gly Pro Phe Thr Ile Leu Lys Lys Phe Leu Ala Ala Thr Asn Asn Lys
 20 25 30
 Glu Asn Val Ser Phe Ile Ala Leu Val His Ser Ala Lys Glu Leu Lys
 35 40 45
 Glu Ser Tyr Pro Trp Val Lys Phe Ile Glu Phe Pro Glu Val Lys Gly
 50 55 60
 Ser Trp Leu Lys Arg Leu His Phe Glu Tyr Val Val Cys Lys Lys Leu
 65 70 75 80
 Ser Lys Glu Leu Asn Ala Thr His Trp Ile Cys Leu His Asp Ile Thr
 85 90 95
 Ala Asn Val Val Thr Lys Lys Arg Tyr Val Tyr Cys His Asn Pro Ala
 100 105 110

Pro Phe Tyr Lys Gly Ile Leu Phe Arg Glu Ile Leu Met Glu Pro Ser
 115 120 125
 Phe Phe Leu Phe Lys Met Leu Tyr Gly Leu Ile Tyr Lys Ile Asn Ile
 130 135 140
 Lys Lys Asn Thr Ala Val Phe Val Gln Gln Phe Trp Met Lys Glu Lys
 145 150 155 160
 Phe Ile Lys Lys Tyr Ser Ile Asn Asn Ile Ile Val Ser Arg Pro Glu
 165 170 175
 Ile Lys Leu Ser Asp Lys Ser Gln Leu Thr Asp Asp Asp Ser Gln Phe
 180 185 190
 Lys Asn Asn Pro Ser Glu Leu Thr Ile Phe Tyr Pro Ala Val Pro Arg
 195 200 205
 Val Phe Lys Asn Tyr Glu Leu Ile Ile Ser Ala Ala Arg Lys Leu Lys
 210 215 220
 Glu Gln Ser Asn Ile Lys Phe Leu Leu Thr Ile Ser Gly Thr Glu Asn
 225 230 235 240
 Ala Tyr Ala Lys Tyr Ile Ile Ser Leu Ala Glu Gly Leu Asp Asn Val
 245 250 255
 His Phe Leu Gly Tyr Leu Asp Lys Glu Lys Ile Asp His Cys Tyr Asn
 260 265 270
 Ile Ser Asp Ile Val Cys Phe Pro Ser Arg Leu Glu Thr Trp Gly Leu
 275 280 285
 Pro Leu Ser Glu Ala Lys Glu Arg Gly Lys Trp Val Leu Ala Ser Asp
 290 295 300
 Phe Pro Phe Thr Arg Glu Thr Leu Gly Ser Tyr Glu Lys Lys Ala Phe
 305 310 315 320
 Phe Asp Ser Asn Asn Asp Asp Met Leu Val Lys Leu Ile Ile Asp Phe
 325 330 335
 Lys Lys Gly Asn Leu Lys Lys Asp Ile Ser Asp Ala Asn Phe Ile Tyr
 340 345 350
 Arg Asn Glu Asn Val Leu Val Gly Phe Asp Glu Leu Val Asn Phe Ile
 355 360 365
 Thr Glu Glu His
 370

<210> 376
 <211> 196
 <212> PRT
 <213> E. Coli

<400> 376

Met Ile Leu Lys Leu Ala Lys Arg Tyr Gly Leu Cys Gly Phe Ile Arg
 1 5 10 15
 Leu Val Arg Asp Val Leu Leu Thr Arg Val Phe Tyr Arg Asn Cys Arg
 20 25 30
 Ile Ile Arg Phe Pro Cys Tyr Ile Arg Asn Asp Gly Ser Ile Asn Phe
 35 40 45
 Gly Glu Asn Phe Thr Ser Gly Val Gly Leu Arg Leu Asp Ala Phe Gly
 50 55 60
 Arg Gly Val Ile Phe Phe Ser Asp Asn Val Gln Val Asn Asp Tyr Val
 65 70 75 80
 His Ile Ala Ser Ile Glu Ser Val Thr Ile Gly Arg Asp Thr Leu Ile
 85 90 95
 Ala Ser Lys Val Phe Ile Thr Asp His Asn His Gly Ser Phe Lys His
 100 105 110
 Ser Asp Pro Met Ser Ser Pro Asn Ile Pro Pro Asp Met Arg Thr Leu

115	120	125
Glu Ser Ser Ala Val Val Ile Gly Gln Arg Val Trp Leu Gly Glu Asn		
130	135	140
Val Thr Val Leu Pro Gly Thr Ile Ile Gly Asn Gly Val Val Val Gly		
145	150	155
Ala Asn Ser Val Val Arg Gly Ser Ile Pro Glu Asn Thr Val Ile Ala		
165	170	175
Gly Val Pro Ala Lys Ile Ile Lys Lys Tyr Asn His Glu Thr Lys Leu		
180	185	190
Trp Glu Lys Ala		
195		

<210> 377

<211> 330

<212> PRT

<213> E. Coli

<400> 377

Met Tyr Phe Leu Asn Asp Leu Asn Phe Ser Arg Arg Asp Ala Gly Phe		
1	5	10
Lys Ala Arg Lys Asp Ala Leu Asp Ile Ala Ser Asp Tyr Glu Asn Ile		
20	25	30
Ser Val Val Asn Ile Pro Leu Trp Gly Gly Val Val Gln Arg Ile Ile		
35	40	45
Ser Ser Val Lys Leu Ser Thr Phe Leu Cys Gly Leu Glu Asn Lys Asp		
50	55	60
Val Leu Ile Phe Asn Phe Pro Met Ala Lys Pro Phe Trp His Ile Leu		
65	70	75
Ser Phe Phe His Arg Leu Leu Lys Phe Arg Ile Val Pro Leu Ile His		
85	90	95
Asp Ile Asp Glu Leu Arg Gly Gly Ser Asp Ser Val Arg Leu		
100	105	110
Ala Thr Cys Asp Met Val Ile Ser His Asn Pro Gln Met Thr Lys Tyr		
115	120	125
Leu Ser Lys Tyr Met Ser Gln Asp Lys Ile Lys Asp Ile Lys Ile Phe		
130	135	140
Asp Tyr Leu Val Ser Ser Asp Val Glu His Arg Asp Val Thr Asp Lys		
145	150	155
Gln Arg Gly Val Ile Tyr Ala Gly Asn Leu Ser Arg His Lys Cys Ser		
165	170	175
Phe Ile Tyr Thr Glu Gly Cys Asp Phe Thr Leu Phe Gly Val Asn Tyr		
180	185	190
Glu Asn Lys Asp Asn Pro Lys Tyr Leu Gly Ser Phe Asp Ala Gln Ser		
195	200	205
Pro Glu Lys Ile Asn Leu Pro Gly Met Gln Phe Gly Leu Ile Trp Asp		
210	215	220
Gly Asp Ser Val Glu Thr Cys Ser Gly Ala Phe Gly Asp Tyr Leu Lys		
225	230	235
Phe Asn Asn Pro His Lys Thr Ser Leu Tyr Leu Ser Met Glu Leu Pro		
245	250	255
Val Phe Ile Trp Asp Lys Ala Ala Leu Ala Asp Phe Ile Val Asp Asn		
260	265	270
Arg Ile Gly Tyr Ala Val Gly Ser Ile Lys Glu Met Gln Glu Ile Val		
275	280	285
Asp Ser Met Thr Ile Glu Thr Tyr Lys Gln Ile Ser Glu Asn Thr Lys		
290	295	300
Ile Ile Ser Gln Lys Ile Arg Thr Gly Ser Tyr Phe Arg Asp Val Leu		

305	310	315	320						
Glu	Glu	Val	Ile	Asp	Asp	Leu	Lys	Thr	Arg
				325				330	

<210> 378
<211> 388
<212> PRT
<213> E. Col

<400> 378

Met	Ile	Tyr	Leu	Val	Ile	Ser	Val	Phe	Leu	Ile	Thr	Ala	Phe	Ile	Cys
1					5				10					15	
Leu	Tyr	Leu	Lys	Lys	Asp	Ile	Phe	Tyr	Pro	Ala	Val	Cys	Val	Asn	Ile
					20			25					30		
Ile	Phe	Ala	Leu	Val	Leu	Leu	Gly	Tyr	Glu	Ile	Thr	Ser	Asp	Ile	Tyr
					35			40				45			
Ala	Phe	Gln	Leu	Asn	Asp	Ala	Thr	Leu	Ile	Phe	Leu	Leu	Cys	Asn	Val
					50			55			60				
Leu	Thr	Phe	Thr	Leu	Ser	Cys	Leu	Leu	Thr	Glu	Ser	Val	Leu	Asp	Leu
					65			70			75			80	
Asn	Ile	Arg	Lys	Val	Asn	Asn	Ala	Ile	Tyr	Ser	Ile	Pro	Ser	Lys	Lys
					85			90				95			
Val	His	Asn	Val	Gly	Leu	Leu	Val	Ile	Ser	Phe	Ser	Met	Ile	Tyr	Ile
					100			105				110			
Cys	Met	Arg	Leu	Ser	Asn	Tyr	Gln	Phe	Gly	Thr	Ser	Leu	Leu	Ser	Tyr
					115			120				125			
Met	Asn	Leu	Ile	Arg	Asp	Ala	Asp	Val	Glu	Asp	Thr	Ser	Arg	Asn	Phe
					130			135			140				
Ser	Ala	Tyr	Met	Gln	Pro	Ile	Ile	Leu	Thr	Thr	Phe	Ala	Leu	Phe	Ile
					145			150			155			160	
Trp	Ser	Lys	Lys	Phe	Thr	Asn	Thr	Lys	Val	Ser	Lys	Thr	Phe	Thr	Leu
					165			170				175			
Leu	Val	Phe	Ile	Val	Phe	Ile	Phe	Ala	Ile	Ile	Leu	Asn	Thr	Gly	Lys
					180			185				190			
Gln	Ile	Val	Phe	Met	Val	Ile	Ile	Ser	Tyr	Ala	Phe	Ile	Val	Gly	Val
					195			200				205			
Asn	Arg	Val	Lys	His	Tyr	Val	Tyr	Leu	Ile	Thr	Ala	Val	Gly	Val	Leu
					210			215			220				
Phe	Ser	Leu	Tyr	Met	Leu	Phe	Leu	Arg	Gly	Leu	Pro	Gly	Gly	Met	Ala
					225			230			235			240	
Tyr	Tyr	Leu	Ser	Met	Tyr	Leu	Val	Ser	Pro	Ile	Ile	Ala	Phe	Gln	Glu
					245			250				255			
Phe	Tyr	Phe	Gln	Gln	Val	Ser	Asn	Ser	Ala	Ser	Ser	His	Val	Phe	Trp
					260			265				270			
Phe	Phe	Glu	Arg	Leu	Met	Gly	Leu	Leu	Thr	Gly	Gly	Val	Ser	Met	Ser
					275			280			285				
Leu	His	Lys	Glu	Phe	Val	Trp	Val	Gly	Leu	Pro	Thr	Asn	Val	Tyr	Thr
					290			295			300				
Ala	Phe	Ser	Asp	Tyr	Val	Tyr	Ile	Ser	Ala	Glu	Leu	Ser	Tyr	Leu	Met
					305			310			315			320	
Met	Val	Ile	His	Gly	Cys	Ile	Ser	Gly	Val	Leu	Trp	Arg	Leu	Ser	Arg
					325			330				335			
Asn	Tyr	Ile	Ser	Val	Lys	Ile	Phe	Tyr	Ser	Tyr	Phe	Ile	Tyr	Thr	Phe
					340			345				350			
Ser	Phe	Ile	Phe	Tyr	His	Glu	Ser	Phe	Met	Thr	Asn	Ile	Ser	Ser	Trp
					355			360			365				

Ile Gln Ile Thr Leu Cys Ile Ile Val Phe Ser Gln Phe Leu Lys Ala
 370 375 380
 Gln Lys Ile Lys
 385

<210> 379
 <211> 367
 <212> PRT
 <213> E. Coli

<400> 379
 Met Tyr Asp Tyr Ile Ile Val Gly Ser Gly Leu Phe Gly Ala Val Cys
 1 5 10 15
 Ala Asn Glu Leu Lys Lys Leu Asn Lys Lys Val Leu Val Ile Glu Lys
 20 25 30
 Arg Asn His Ile Gly Gly Asn Ala Tyr Thr Glu Asp Cys Glu Gly Ile
 35 40 45
 Gln Ile His Lys Tyr Gly Ala His Ile Phe His Thr Asn Asp Lys Tyr
 50 55 60
 Ile Trp Asp Tyr Val Asn Asp Leu Val Glu Phe Asn Arg Phe Thr Asn
 65 70 75 80
 Ser Pro Leu Ala Ile Tyr Lys Asp Lys Leu Phe Asn Leu Pro Phe Asn
 85 90 95
 Met Asn Thr Phe His Gln Met Trp Gly Val Lys Asp Pro Gln Glu Ala
 100 105 110
 Gln Asn Ile Ile Asn Ala Gln Lys Lys Tyr Gly Asp Lys Val Pro
 115 120 125
 Glu Asn Leu Glu Glu Gln Ala Ile Ser Leu Val Gly Glu Asp Leu Tyr
 130 135 140
 Gln Ala Leu Ile Lys Gly Tyr Thr Glu Lys Gln Trp Gly Arg Ser Ala
 145 150 155 160
 Lys Glu Leu Pro Ala Phe Ile Ile Lys Arg Ile Pro Val Arg Phe Thr
 165 170 175
 Phe Asp Asn Asn Tyr Phe Ser Asp Arg Tyr Gln Gly Ile Pro Val Gly
 180 185 190
 Gly Tyr Thr Lys Leu Ile Glu Lys Met Leu Glu Gly Val Asp Val Lys
 195 200 205
 Leu Gly Ile Asp Phe Leu Lys Asp Lys Asp Ser Leu Ala Ser Lys Ala
 210 215 220
 His Arg Ile Ile Tyr Thr Gly Pro Ile Asp Gln Tyr Phe Asp Tyr Arg
 225 230 235 240
 Phe Gly Ala Leu Glu Tyr Arg Ser Leu Lys Phe Glu Thr Glu Arg His
 245 250 255
 Glu Phe Pro Asn Phe Gln Gly Asn Ala Val Ile Asn Phe Thr Asp Ala
 260 265 270
 Asn Val Pro Tyr Thr Arg Ile Ile Glu His Lys His Phe Asp Tyr Val
 275 280 285
 Glu Thr Lys His Thr Val Val Thr Lys Glu Tyr Pro Leu Glu Trp Lys
 290 295 300
 Val Gly Asp Glu Pro Tyr Tyr Pro Val Asn Asp Asn Lys Asn Met Glu
 305 310 315 320
 Leu Phe Lys Lys Tyr Arg Glu Leu Ala Ser Arg Glu Asp Lys Val Ile
 325 330 335
 Phe Gly Gly Arg Leu Ala Glu Tyr Lys Tyr Tyr Asp Met His Gln Val
 340 345 350

Ile Ser Ala Ala Leu Tyr Gln Val Lys Asn Ile Met Ser Thr Asp
355 360 365

<210> 380

<211> 371

<212> PRT

<213> E. Coli

<400> 380

Met Phe Pro Lys Ile Met Asn Asp Glu Asn Phe Phe Lys Lys Ala Ala
1 5 10 15
Ala His Gly Glu Glu Pro Pro Leu Thr Pro Gln Asn Glu His Gln Arg
20 25 30
Ser Gly Leu Arg Phe Ala Arg Arg Val Arg Leu Pro Arg Ala Val Gly
35 40 45
Leu Ala Gly Met Phe Leu Pro Ile Ala Ser Thr Leu Val Ser His Pro
50 55 60
Pro Pro Gly Trp Trp Trp Leu Val Leu Val Gly Trp Ala Phe Val Trp
65 70 75 80
Pro His Leu Ala Trp Gln Ile Ala Ser Arg Ala Val Asp Pro Leu Ser
85 90 95
Arg Glu Ile Tyr Asn Leu Lys Thr Asp Ala Val Leu Ala Gly Met Trp
100 105 110
Val Gly Val Met Gly Val Asn Val Leu Pro Ser Thr Ala Met Leu Met
115 120 125
Ile Met Cys Leu Asn Leu Met Gly Ala Gly Gly Pro Arg Leu Phe Val
130 135 140
Ala Gly Leu Val Leu Met Val Val Ser Cys Leu Val Thr Leu Glu Leu
145 150 155 160
Thr Gly Ile Thr Val Ser Phe Asn Ser Ala Pro Leu Glu Trp Trp Leu
165 170 175
Ser Leu Pro Ile Ile Val Ile Tyr Pro Leu Leu Phe Gly Trp Val Ser
180 185 190
Tyr Gln Thr Ala Thr Lys Leu Ala Glu His Lys Arg Arg Leu Gln Val
195 200 205
Met Ser Thr Arg Asp Gly Met Thr Gly Val Tyr Asn Arg Arg His Trp
210 215 220
Glu Thr Met Leu Arg Asn Glu Phe Asp Asn Cys Arg Arg His Asn Arg
225 230 235 240
Asp Ala Thr Leu Leu Ile Ile Asp Ile Asp His Phe Lys Ser Ile Asn
245 250 255
Asp Thr Trp Gly His Asp Val Gly Asp Glu Ala Ile Val Ala Leu Thr
260 265 270
Arg Gln Leu Gln Ile Thr Leu Arg Gly Ser Asp Val Ile Gly Arg Phe
275 280 285
Gly Gly Asp Glu Phe Ala Val Ile Met Ser Gly Thr Pro Ala Glu Ser
290 295 300
Ala Ile Thr Ala Met Leu Arg Val His Glu Gly Leu Asn Thr Leu Arg
305 310 315 320
Leu Pro Asn Thr Pro Gln Val Thr Leu Arg Ile Ser Val Gly Val Ala
325 330 335
Pro Leu Asn Pro Gln Met Ser His Tyr Arg Glu Trp Leu Lys Ser Ala
340 345 350
Asp Leu Ala Leu Tyr Lys Ala Lys Lys Ala Gly Arg Asn Arg Thr Glu
355 360 365
Val Ala Ala

<210> 381
 <211> 467
 <212> PRT
 <213> E. Coli

<400> 381
 Met Asp Val Asn Val Asp Gln Phe Asp Thr Glu Ala Phe Arg Thr Asp
 1 5 10 15
 Lys Leu Glu Leu Thr Ser Gly Asn Ile Ala Asp His Asn Gly Asn Val
 20 25 30
 Val Ser Gly Val Phe Asp Ile His Ser Ser Asp Tyr Val Leu Asn Ala
 35 40 45
 Asp Leu Val Asn Asp Arg Thr Trp Asp Thr Ser Lys Ser Asn Tyr Gly
 50 55 60
 Tyr Gly Ile Val Ala Met Asn Ser Asp Gly His Leu Thr Ile Asn Gly
 65 70 75 80
 Asn Gly Asp Val Asp Asn Gly Thr Glu Leu Asp Asn Ser Ser Val Asp
 85 90 95
 Asn Val Val Ala Ala Thr Gly Asn Tyr Lys Val Arg Ile Asp Asn Ala
 100 105 110
 Thr Gly Ala Gly Ala Ile Ala Asp Tyr Lys Asp Lys Glu Ile Ile Tyr
 115 120 125
 Val Asn Asp Val Asn Ser Asn Ala Thr Phe Ser Ala Ala Asn Lys Ala
 130 135 140
 Asp Leu Gly Ala Tyr Thr Tyr Gln Ala Glu Gln Arg Gly Asn Thr Val
 145 150 155 160
 Val Leu Gln Gln Met Glu Leu Thr Asp Tyr Ala Asn Met Ala Leu Ser
 165 170 175
 Ile Pro Ser Ala Asn Thr Asn Ile Trp Asn Leu Glu Gln Asp Thr Val
 180 185 190
 Gly Thr Arg Leu Thr Asn Ser Arg His Gly Leu Ala Asp Asn Gly Gly
 195 200 205
 Ala Trp Val Ser Tyr Phe Gly Gly Asn Phe Asn Gly Asp Asn Gly Thr
 210 215 220
 Ile Asn Tyr Asp Gln Asp Val Asn Gly Ile Met Val Gly Val Asp Thr
 225 230 235 240
 Lys Ile Asp Gly Asn Asn Ala Lys Trp Ile Val Gly Ala Ala Gly
 245 250 255
 Phe Ala Lys Gly Asp Met Asn Asp Arg Ser Gly Gln Val Asp Gln Asp
 260 265 270
 Ser Gln Thr Ala Tyr Ile Tyr Ser Ser Ala His Phe Ala Asn Asn Val
 275 280 285
 Phe Val Asp Gly Ser Leu Ser Tyr Ser His Phe Asn Asn Asp Leu Ser
 290 295 300
 Ala Thr Met Ser Asn Gly Thr Tyr Val Asp Gly Ser Thr Asn Ser Asp
 305 310 315 320
 Ala Trp Gly Phe Gly Leu Lys Ala Gly Tyr Asp Phe Lys Leu Gly Asp
 325 330 335
 Ala Gly Tyr Val Thr Pro Tyr Gly Ser Val Ser Gly Leu Phe Gln Ser
 340 345 350
 Gly Asp Asp Tyr Gln Leu Ser Asn Asp Met Lys Val Asp Gly Gln Ser
 355 360 365
 Tyr Asp Ser Met Arg Tyr Glu Leu Gly Val Asp Ala Gly Tyr Thr Phe
 370 375 380
 Thr Tyr Ser Glu Asp Gln Ala Leu Thr Pro Tyr Phe Lys Leu Ala Tyr

385	390	395	400
Val	Tyr Asp Asp Ser Asn Asn Asp Asn	Asp Val Asn Gly Asp Ser Ile	
	405	410	415
Asp Asn Gly Thr Glu Gly Ser Ala Val Arg Val Gly Leu Gly Thr Gln			
	420	425	430
Phe Ser Phe Thr Lys Asn Phe Ser Ala Tyr Thr Asp Ala Asn Tyr Leu			
	435	440	445
Gly Gly Gly Asp Val Asp Gln Asp Trp Ser Ala Asn Val Gly Val Lys			
	450	455	460
Tyr Thr Trp			
	465		

<210> 382
<211> 222
<212> PRT
<213> E. Coli

<400> 382			
Met Pro Val Lys Asp Leu Thr Gly Ile Thr Ala Lys Asp Ala Gln Met			
1	5	10	15
Leu Ser Val Val Lys Pro Leu Gln Glu Phe Gly Lys Leu Asp Lys Cys			
20	25	30	
Leu Ser Arg Tyr Gly Thr Arg Phe Glu Phe Asn Asn Glu Lys Gln Val			
35	40	45	
Ile Phe Ser Ser Asp Val Asn Asn Glu Asp Thr Phe Val Ile Leu Glu			
50	55	60	
Gly Val Ile Ser Leu Arg Arg Glu Glu Asn Val Leu Ile Gly Ile Thr			
65	70	75	80
Gln Ala Pro Tyr Ile Met Gly Leu Ala Asp Gly Leu Met Lys Asn Asp			
85	90	95	
Ile Pro Tyr Lys Leu Ile Ser Glu Gly Asn Cys Thr Gly Tyr His Leu			
100	105	110	
Pro Ala Lys Gln Thr Ile Thr Leu Ile Glu Gln Asn Gln Leu Trp Arg			
115	120	125	
Asp Ala Phe Tyr Trp Leu Ala Trp Gln Asn Arg Ile Leu Glu Leu Arg			
130	135	140	
Asp Val Gln Leu Ile Gly His Asn Ser Tyr Glu Gln Ile Arg Ala Thr			
145	150	155	160
Leu Leu Ser Met Ile Asp Trp Asn Glu Glu Leu Arg Ser Arg Ile Gly			
165	170	175	
Val Met Asn Tyr Ile His Gln Arg Thr Arg Ile Ser Arg Ser Val Val			
180	185	190	
Ala Glu Val Leu Ala Ala Leu Arg Lys Gly Gly Tyr Ile Glu Met Asn			
195	200	205	
Lys Gly Lys Leu Val Ala Ile Asn Arg Leu Pro Ser Glu Tyr			
210	215	220	

<210> 383
<211> 84
<212> PRT
<213> E. Coli

<400> 383

Met Thr Asp Lys Ile Arg Thr Leu Gln Gly Arg Val Val Ser Asp Lys

1	5	10	15												
Met	Glu	Lys	Ser	Ile	Val	Val	Ala	Ile	Glu	Arg	Phe	Val	Lys	His	Pro
				20				25						30	
Ile	Tyr	Gly	Lys	Phe	Ile	Lys	Arg	Thr	Thr	Lys	Leu	His	Val	His	Asp
				35			40			45					
Glu	Asn	Asn	Glu	Cys	Gly	Ile	Gly	Asp	Val	Val	Glu	Ile	Arg	Glu	Cys
				50			55			60					
Arg	Pro	Leu	Ser	Lys	Thr	Lys	Ser	Trp	Thr	Leu	Val	Arg	Val	Val	Glu
				65			70			75			80		
Lys	Ala	Val	Leu												

<210> 384

<211> 63

<212> PRT

<213> E. Coli

<400> 384

Met	Lys	Ala	Lys	Glu	Leu	Arg	Glu	Lys	Ser	Val	Glu	Glu	Leu	Asn	Thr
1				5				10						15	
Glu	Leu	Leu	Asn	Leu	Leu	Arg	Glu	Gln	Phe	Asn	Leu	Arg	Met	Gln	Ala
				20				25					30		
Ala	Ser	Gly	Gln	Leu	Gln	Gln	Ser	His	Leu	Leu	Lys	Gln	Val	Arg	Arg
				35			40				45				
Asp	Val	Ala	Arg	Val	Lys	Thr	Leu	Leu	Asn	Glu	Lys	Ala	Gly	Ala	
				50			55			60					

<210> 385

<211> 136

<212> PRT

<213> E. Coli

<400> 385

Met	Leu	Gln	Pro	Lys	Arg	Thr	Lys	Phe	Arg	Lys	Met	His	Lys	Gly	Arg
1					5				10				15		
Asn	Arg	Gly	Leu	Ala	Gln	Gly	Thr	Asp	Val	Ser	Phe	Gly	Ser	Phe	Gly
					20				25			30			
Leu	Lys	Ala	Val	Gly	Arg	Gly	Arg	Leu	Thr	Ala	Arg	Gln	Ile	Glu	Ala
					35			40			45				
Ala	Arg	Arg	Ala	Met	Thr	Arg	Ala	Val	Lys	Arg	Gln	Gly	Lys	Ile	Trp
					50			55			60				
Ile	Arg	Val	Phe	Pro	Asp	Lys	Pro	Ile	Thr	Glu	Lys	Pro	Leu	Ala	Val
					65			70			75		80		
Arg	Met	Gly	Lys	Gly	Lys	Gly	Asn	Val	Glu	Tyr	Trp	Val	Ala	Leu	Ile
					85			90			95				
Gln	Pro	Gly	Lys	Val	Leu	Tyr	Glu	Met	Asp	Gly	Val	Pro	Glu	Glu	Leu
					100			105			110				
Ala	Arg	Glu	Ala	Phe	Lys	Leu	Ala	Ala	Ala	Lys	Leu	Pro	Ile	Lys	Thr
					115			120			125				
Thr	Phe	Val	Thr	Lys	Thr	Val	Met								
					130		135								

<210> 386

<211> 233

<212> PRT
<213> E. Coli

<400> 386

Met Gly Gln Lys Val His Pro Asn Gly Ile Arg Leu Gly Ile Val Lys
1 5 10 15
Pro Trp Asn Ser Thr Trp Phe Ala Asn Thr Lys Glu Phe Ala Asp Asn
20 25 30
Leu Asp Ser Asp Phe Lys Val Arg Gln Tyr Leu Thr Lys Glu Leu Ala
35 40 45
Lys Ala Ser Val Ser Arg Ile Val Ile Glu Arg Pro Ala Lys Ser Ile
50 55 60
Arg Val Thr Ile His Thr Ala Arg Pro Gly Ile Val Ile Gly Lys Lys
65 70 75 80
Gly Glu Asp Val Glu Lys Leu Arg Lys Val Val Ala Asp Ile Ala Gly
85 90 95
Val Pro Ala Gln Ile Asn Ile Ala Glu Val Arg Lys Pro Glu Leu Asp
100 105 110
Ala Lys Leu Val Ala Asp Ser Ile Thr Ser Gln Leu Glu Arg Arg Val
115 120 125
Met Phe Arg Arg Ala Met Lys Arg Ala Val Gln Asn Ala Met Arg Leu
130 135 140
Gly Ala Lys Gly Ile Lys Val Glu Val Ser Gly Arg Leu Gly Gly Ala
145 150 155 160
Glu Ile Ala Arg Thr Glu Trp Tyr Arg Glu Gly Arg Val Pro Leu His
165 170 175
Thr Leu Arg Ala Asp Ile Asp Tyr Asn Thr Ser Glu Ala His Thr Thr
180 185 190
Tyr Gly Val Ile Gly Val Lys Val Trp Ile Phe Lys Gly Glu Ile Leu
195 200 205
Gly Gly Met Ala Ala Val Glu Gln Pro Glu Lys Pro Ala Ala Gln Pro
210 215 220
Lys Lys Gln Gln Arg Lys Gly Arg Lys
225 230

<210> 387
<211> 110
<212> PRT
<213> E. Coli

<400> 387

Met Glu Thr Ile Ala Lys His Arg His Ala Arg Ser Ser Ala Gln Lys
1 5 10 15
Val Arg Leu Val Ala Asp Leu Ile Arg Gly Lys Lys Val Ser Gln Ala
20 25 30
Leu Asp Ile Leu Thr Tyr Thr Asn Lys Lys Ala Ala Val Leu Val Lys
35 40 45
Lys Val Leu Glu Ser Ala Ile Ala Asn Ala Glu His Asn Asp Gly Ala
50 55 60
Asp Ile Asp Asp Leu Lys Val Thr Lys Ile Phe Val Asp Glu Gly Pro
65 70 75 80
Ser Met Lys Arg Ile Met Pro Arg Ala Lys Gly Arg Ala Asp Arg Ile
85 90 95
Leu Lys Arg Thr Ser His Ile Thr Val Val Val Ser Asp Arg
100 105 110

<210> 388
<211> 92
<212> PRT
<213> E. Coli

<400> 388
Met Pro Arg Ser Leu Lys Lys Gly Pro Phe Ile Asp Leu His Leu Leu
1 5 10 15
Met Lys Val Glu Lys Ala Val Glu Ser Gly Asp Lys Lys Pro Leu Arg
20 25 30
Thr Trp Ser Arg Arg Ser Thr Ile Phe Pro Asn Met Ile Gly Leu Thr
35 40 45
Ile Ala Val His Asn Gly Arg Gln His Val Pro Val Phe Val Thr Asp
50 55 60
Glu Met Val Gly His Lys Leu Gly Glu Phe Ala Pro Thr Arg Thr Tyr
65 70 75 80
Arg Gly His Ala Ala Asp Lys Lys Ala Lys Lys Lys
85 90

<210> 389
<211> 273
<212> PRT
<213> E. Coli

<400> 389
Met Ala Val Val Lys Cys Lys Pro Thr Ser Pro Gly Arg Arg His Val
1 5 10 15
Val Lys Val Val Asn Pro Glu Leu His Lys Gly Lys Pro Phe Ala Pro
20 25 30
Leu Leu Glu Lys Asn Ser Lys Ser Gly Gly Arg Asn Asn Asn Gly Arg
35 40 45
Ile Thr Thr Arg His Ile Gly Gly His Lys Gln Ala Tyr Arg Ile
50 55 60
Val Asp Phe Lys Arg Asn Lys Asp Gly Ile Pro Ala Val Val Glu Arg
65 70 75 80
Leu Glu Tyr Asp Pro Asn Arg Ser Ala Asn Ile Ala Leu Val Leu Tyr
85 90 95
Lys Asp Gly Glu Arg Arg Tyr Ile Leu Ala Pro Lys Gly Leu Lys Ala
100 105 110
Gly Asp Gln Ile Gln Ser Gly Val Asp Ala Ala Ile Lys Pro Gly Asn
115 120 125
Thr Leu Pro Met Arg Asn Ile Pro Val Gly Ser Thr Val His Asn Val
130 135 140
Glu Met Lys Pro Gly Lys Gly Gln Leu Ala Arg Ser Ala Gly Thr
145 150 155 160
Tyr Val Gln Ile Val Ala Arg Asp Gly Ala Tyr Val Thr Leu Arg Leu
165 170 175
Arg Ser Gly Glu Met Arg Lys Val Glu Ala Asp Cys Arg Ala Thr Leu
180 185 190
Gly Glu Val Gly Asn Ala Glu His Met Leu Arg Val Leu Gly Lys Ala
195 200 205
Gly Ala Ala Arg Trp Arg Gly Val Arg Pro Thr Val Arg Gly Thr Ala

210	215	220
Met Asn Pro Val Asp His Pro His Gly Gly Gly Glu Gly Arg Asn Phe		
225	230	235
Gly Lys His Pro Val Thr Pro Trp Gly Val Gln Thr Lys Gly Lys Lys		240
245	250	255
Thr Arg Ser Asn Lys Arg Thr Asp Lys Phe Ile Val Arg Arg Arg Ser		
260	265	270
Lys		

<210> 390
<211> 100
<212> PRT
<213> E. Coli

<400> 390		
Met Ile Arg Glu Glu Arg Leu Leu Lys Val Leu Arg Ala Pro His Val		
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Ser Glu Lys Ala Ser Thr Ala Met Glu Lys Ser Asn Thr Ile Val Leu		15
20	25	30
Lys Val Ala Lys Asp Ala Thr Lys Ala Glu Ile Lys Ala Ala Val Gln		
35	40	45
Lys Leu Phe Glu Val Glu Val Val Asn Thr Leu Val Val Lys		
50	55	60
Gly Lys Val Lys Arg His Gly Gln Arg Ile Gly Arg Arg Ser Asp Trp		
65	70	75
80		
Lys Lys Ala Tyr Val Thr Leu Lys Glu Gly Gln Asn Leu Asp Phe Val		
85	90	95
Gly Gly Ala Glu		
100		

<210> 391
<211> 201
<212> PRT
<213> E. Coli

<400> 391		
Met Glu Leu Val Leu Lys Asp Ala Gln Ser Ala Leu Thr Val Ser Glu		
1	5	10
Thr Thr Phe Gly Arg Asp Phe Asn Glu Ala Leu Val His Gln Val Val		15
20	25	30
Val Ala Tyr Ala Ala Gly Ala Arg Gln Gly Thr Arg Ala Gln Lys Thr		
35	40	45
Arg Ala Glu Val Thr Gly Ser Gly Lys Lys Pro Trp Arg Gln Lys Gly		
50	55	60
Thr Gly Arg Ala Arg Ser Gly Ser Ile Lys Ser Pro Ile Trp Arg Ser		
65	70	75
80		
Gly Gly Val Thr Phe Ala Ala Arg Pro Gln Asp His Ser Gln Lys Val		
85	90	95
Asn Lys Lys Met Tyr Arg Gly Ala Leu Lys Ser Ile Leu Ser Glu Leu		
100	105	110
Val Arg Gln Asp Arg Leu Ile Val Val Glu Lys Phe Ser Val Glu Ala		
115	120	125

Pro Lys Thr Lys Leu Leu Ala Gln Lys Leu Lys Asp Met Ala Leu Glu
 130 135 140
 Asp Val Leu Ile Ile Thr Gly Glu Leu Asp Glu Asn Leu Phe Leu Ala
 145 150 155 160
 Ala Arg Asn Leu His Lys Val Asp Val Arg Asp Ala Thr Gly Ile Asp
 165 170 175
 Pro Val Ser Leu Ile Ala Phe Asp Lys Val Val Met Thr Ala Asp Ala
 180 185 190
 Val Lys Gln Val Glu Glu Met Leu Ala
 195 200

<210> 392
 <211> 209
 <212> PRT
 <213> E. Coli

<400> 392

Met Ile Gly Leu Val Gly Lys Val Gly Met Thr Arg Ile Phe Thr
 1 5 10 15
 Glu Asp Gly Val Ser Ile Pro Val Thr Val Ile Glu Val Glu Ala Asn
 20 25 30
 Arg Val Thr Gln Val Lys Asp Leu Ala Asn Asp Gly Tyr Arg Ala Ile
 35 40 45
 Gln Val Thr Thr Gly Ala Lys Lys Ala Asn Arg Val Thr Lys Pro Glu
 50 55 60
 Ala Gly His Phe Ala Lys Ala Gly Val Glu Ala Gly Arg Gly Leu Trp
 65 70 75 80
 Glu Phe Arg Leu Ala Glu Gly Glu Glu Phe Thr Val Gly Gln Ser Ile
 85 90 95
 Ser Val Glu Leu Phe Ala Asp Val Lys Lys Val Asp Val Thr Gly Thr
 100 105 110
 Ser Lys Gly Lys Gly Phe Ala Gly Thr Val Lys Arg Trp Asn Phe Arg
 115 120 125
 Thr Gln Asp Ala Thr His Gly Asn Ser Leu Ser His Arg Val Pro Gly
 130 135 140
 Ser Ile Gly Gln Asn Gln Thr Pro Gly Lys Val Phe Lys Gly Lys Lys
 145 150 155 160
 Met Ala Gly Gln Met Gly Asn Glu Arg Val Thr Val Gln Ser Leu Asp
 165 170 175
 Val Val Arg Val Asp Ala Glu Arg Asn Leu Leu Leu Val Lys Gly Ala
 180 185 190
 Val Pro Gly Ala Thr Gly Ser Asp Leu Ile Val Lys Pro Ala Val Lys
 195 200 205
 Ala

<210> 393
 <211> 103
 <212> PRT
 <213> E. Coli

<400> 393

Met Gln Asn Gln Arg Ile Arg Ile Arg Leu Lys Ala Phe Asp His Arg

1	5	10	15
Leu Ile Asp Gln Ala Thr Ala Glu Ile Val Glu Thr Ala Lys Arg Thr			
20	25	30	
Gly Ala Gln Val Arg Gly Pro Ile Pro Leu Pro Thr Arg Lys Glu Arg			
35	40	45	
Phe Thr Val Leu Ile Ser Pro His Val Asn Lys Asp Ala Arg Asp Gln			
50	55	60	
Tyr Glu Ile Arg Thr His Leu Arg Leu Val Asp Ile Val Glu Pro Thr			
65	70	75	80
Glu Lys Thr Val Asp Ala Leu Met Arg Leu Asp Leu Ala Ala Gly Val			
85	90	95	
Asp Val Gln Ile Ser Leu Gly			
100			

<210> 394
<211> 118
<212> PRT
<213> E. Coli

<400> 394

Met Ala Arg Val Lys Arg Gly Val Ile Ala Arg Ala Arg His Lys Lys			
1	5	10	15
Ile Leu Lys Gln Ala Lys Gly Tyr Tyr Gly Ala Arg Ser Arg Val Tyr			
20	25	30	
Arg Val Ala Phe Gln Ala Val Ile Lys Ala Gly Gln Tyr Ala Tyr Arg			
35	40	45	
Asp Arg Arg Gln Arg Lys Arg Gln Phe Arg Gln Leu Trp Ile Ala Arg			
50	55	60	
Ile Asn Ala Ala Ala Arg Gln Asn Gly Ile Ser Tyr Ser Lys Phe Ile			
65	70	75	80
Asn Gly Leu Lys Lys Ala Ser Val Glu Ile Asp Arg Lys Ile Leu Ala			
85	90	95	
Asp Ile Ala Val Phe Asp Lys Val Ala Phe Thr Ala Leu Val Glu Lys			
100	105	110	
Ala Lys Ala Ala Leu Ala			
115			

<210> 395
<211> 65
<212> PRT
<213> E. Coli

<400> 395

Met Pro Lys Ile Lys Thr Val Arg Gly Ala Ala Lys Arg Phe Lys Lys			
1	5	10	15
Thr Gly Lys Gly Gly Phe Lys His Lys His Ala Asn Leu Arg His Ile			
20	25	30	
Leu Thr Lys Lys Ala Thr Lys Arg Lys Arg His Leu Arg Pro Lys Ala			
35	40	45	
Met Val Ser Lys Gly Asp Leu Gly Leu Val Ile Ala Cys Leu Pro Tyr			
50	55	60	
Ala			
65			

<210> 396
<211> 180
<212> PRT
<213> E. Coli

<400> 396
Met Lys Gly Gly Lys Arg Val Gln Thr Ala Arg Pro Asn Arg Ile Asn
1 5 10 15
Gly Glu Ile Arg Ala Gln Glu Val Arg Leu Thr Gly Leu Glu Gly Glu
20 25 30
Gln Leu Gly Ile Val Ser Leu Arg Glu Ala Leu Glu Lys Ala Glu Glu
35 40 45
Ala Gly Val Asp Leu Val Glu Ile Ser Pro Asn Ala Glu Pro Pro Val
50 55 60
Cys Arg Ile Met Asp Tyr Gly Lys Phe Leu Tyr Glu Lys Ser Lys Ser
65 70 75 80
Ser Lys Glu Gln Lys Lys Gln Lys Val Ile Gln Val Lys Glu Ile
85 90 95
Lys Phe Arg Pro Gly Thr Asp Glu Gly Asp Tyr Gln Val Lys Leu Arg
100 105 110
Ser Leu Ile Arg Phe Leu Glu Glu Gly Asp Lys Ala Lys Ile Thr Leu
115 120 125
Arg Phe Arg Gly Arg Glu Met Ala His Gln Gln Ile Gly Met Glu Val
130 135 140
Leu Asn Arg Val Lys Asp Asp Leu Gln Glu Leu Ala Val Val Glu Ser
145 150 155 160
Phe Pro Thr Lys Ile Glu Gly Arg Gln Met Ile Met Val Leu Ala Pro
165 170 175
Lys Lys Lys Gln
180

<210> 397
<211> 642
<212> PRT
<213> E. Coli

<400> 397
Met Pro Val Ile Thr Leu Pro Asp Gly Ser Gln Arg His Tyr Asp His
1 5 10 15
Ala Val Ser Pro Met Asp Val Ala Leu Asp Ile Gly Pro Gly Leu Ala
20 25 30
Lys Ala Cys Ile Ala Gly Arg Val Asn Gly Glu Leu Val Asp Ala Cys
35 40 45
Asp Leu Ile Glu Asn Asp Ala Gln Leu Ser Ile Ile Thr Ala Lys Asp
50 55 60
Glu Glu Gly Leu Glu Ile Ile Arg His Ser Cys Ala His Leu Leu Gly
65 70 75 80
His Ala Ile Lys Gln Leu Trp Pro His Thr Lys Met Ala Ile Gly Pro
85 90 95
Val Ile Asp Asn Gly Phe Tyr Tyr Asp Val Asp Leu Asp Arg Thr Leu
100 105 110
Thr Gln Glu Asp Val Glu Ala Leu Glu Lys Arg Met His Glu Leu Ala
115 120 125

Glu Lys Asn Tyr Asp Val Ile Lys Lys Lys Val Ser Trp His Glu Ala
 130 135 140
 Arg Glu Thr Phe Ala Asn Arg Gly Glu Ser Tyr Lys Val Ser Ile Leu
 145 150 155 160
 Asp Glu Asn Ile Ala His Asp Asp Lys Pro Gly Leu Tyr Phe His Glu
 165 170 175
 Glu Tyr Val Asp Met Cys Arg Gly Pro His Val Pro Asn Met Arg Phe
 180 185 190
 Cys His His Phe Lys Leu Met Lys Thr Ala Gly Ala Tyr Trp Arg Gly
 195 200 205
 Asp Ser Asn Asn Lys Met Leu Gln Arg Ile Tyr Gly Thr Ala Trp Ala
 210 215 220
 Asp Lys Lys Ala Leu Asn Ala Tyr Leu Gln Arg Leu Glu Glu Ala Ala
 225 230 235 240
 Lys Arg Asp His Arg Lys Ile Gly Lys Gln Leu Asp Leu Tyr His Met
 245 250 255
 Gln Glu Glu Ala Pro Gly Met Val Phe Trp His Asn Asp Gly Trp Thr
 260 265 270
 Ile Phe Arg Glu Leu Glu Val Phe Val Arg Ser Lys Leu Lys Glu Tyr
 275 280 285
 Gln Tyr Gln Glu Val Lys Gly Pro Phe Met Met Asp Arg Val Leu Trp
 290 295 300
 Glu Lys Thr Gly His Trp Asp Asn Tyr Lys Asp Ala Met Phe Thr Thr
 305 310 315 320
 Ser Ser Glu Asn Arg Glu Tyr Cys Ile Lys Pro Met Asn Cys Pro Gly
 325 330 335
 His Val Gln Ile Phe Asn Gln Gly Leu Lys Ser Tyr Arg Asp Leu Pro
 340 345 350
 Leu Arg Met Ala Glu Phe Gly Ser Cys His Arg Asn Glu Pro Ser Gly
 355 360 365
 Ser Leu His Gly Leu Met Arg Val Arg Gly Phe Thr Gln Asp Asp Ala
 370 375 380
 His Ile Phe Cys Thr Glu Glu Gln Ile Arg Asp Glu Val Asn Gly Cys
 385 390 395 400
 Ile Arg Leu Val Tyr Asp Met Tyr Ser Thr Phe Gly Phe Glu Lys Ile
 405 410 415
 Val Val Lys Leu Ser Thr Arg Pro Glu Lys Arg Ile Gly Ser Asp Glu
 420 425 430
 Met Trp Asp Arg Ala Glu Ala Asp Leu Ala Val Ala Leu Glu Glu Asn
 435 440 445
 Asn Ile Pro Phe Glu Tyr Gln Leu Gly Glu Gly Ala Phe Tyr Gly Pro
 450 455 460
 Lys Ile Glu Phe Thr Leu Tyr Asp Cys Leu Asp Arg Ala Trp Gln Cys
 465 470 475 480
 Gly Thr Val Gln Leu Asp Phe Ser Leu Pro Ser Arg Leu Ser Ala Ser
 485 490 495
 Tyr Val Gly Glu Asp Asn Glu Arg Lys Val Pro Val Met Ile His Arg
 500 505 510
 Ala Ile Leu Gly Ser Met Glu Arg Phe Ile Gly Ile Leu Thr Glu Glu
 515 520 525
 Phe Ala Gly Phe Phe Pro Thr Trp Leu Ala Pro Val Gln Val Val Ile
 530 535 540
 Met Asn Ile Thr Asp Ser Gln Ser Glu Tyr Val Asn Glu Leu Thr Gln
 545 550 555 560
 Lys Leu Ser Asn Ala Gly Ile Arg Val Lys Ala Asp Leu Arg Asn Glu
 565 570 575
 Lys Ile Gly Phe Lys Ile Arg Glu His Thr Leu Arg Arg Val Pro Tyr

	580		585		590										
Met	Leu	Val	Cys	Gly	Asp	Lys	Glu	Val	Glu	Ser	Gly	Lys	Val	Ala	Val
	595					600							605		
Arg	Thr	Arg	Arg	Gly	Lys	Asp	Leu	Gly	Ser	Met	Asp	Val	Asn	Glu	Val
	610					615							620		
Ile	Glu	Lys	Leu	Gln	Gln	Glu	Ile	Arg	Ser	Arg	Ser	Leu	Lys	Gln	Leu
	625					630					635				640
Glu	Glu														

<210> 398
<211> 450
<212> PRT
<213> E. Coli

	<400> 398														
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									20		25			30	
Ile	Glu	Ala	Lys	Glu	Leu	Gly	Gly	Thr	Cys	Val	Asn	Val	Gly	Cys	Val
	35					40						45			
Pro	Lys	Lys	Val	Met	Trp	His	Ala	Ala	Gln	Ile	Arg	Glu	Ala	Ile	His
	50					55					60				
Met	Tyr	Gly	Pro	Asp	Tyr	Gly	Phe	Asp	Thr	Thr	Ile	Asn	Lys	Phe	Asn
	65					70				75				80	
Trp	Glu	Thr	Leu	Ile	Ala	Ser	Arg	Thr	Ala	Tyr	Ile	Asp	Arg	Ile	His
	85							90					95		
Thr	Ser	Tyr	Glu	Asn	Val	Leu	Gly	Lys	Asn	Asn	Val	Asp	Val	Ile	Lys
	100					105						110			
Gly	Phe	Ala	Arg	Phe	Val	Asp	Ala	Lys	Thr	Leu	Glu	Val	Asn	Gly	Glu
	115					120						125			
Thr	Ile	Thr	Ala	Asp	His	Ile	Leu	Ile	Ala	Thr	Gly	Gly	Arg	Pro	Ser
	130					135					140				
His	Pro	Asp	Ile	Pro	Gly	Val	Glu	Tyr	Gly	Ile	Asp	Ser	Asp	Gly	Phe
	145					150				155			160		
Phe	Ala	Leu	Pro	Ala	Leu	Pro	Glu	Arg	Val	Ala	Val	Val	Gly	Ala	Gly
	165					170						175			
Tyr	Ile	Ala	Val	Glu	Leu	Ala	Gly	Val	Ile	Asn	Gly	Leu	Gly	Ala	Lys
	180					185						190			
Thr	His	Leu	Phe	Val	Arg	Lys	His	Ala	Pro	Leu	Arg	Ser	Phe	Asp	Pro
	195					200					205				
Met	Ile	Ser	Glu	Thr	Leu	Val	Glu	Val	Met	Asn	Ala	Glu	Gly	Pro	Gln
	210					215					220				
Leu	His	Thr	Asn	Ala	Ile	Pro	Lys	Ala	Val	Val	Lys	Asn	Thr	Asp	Gly
	225					230				235			240		
Ser	Leu	Thr	Leu	Glu	Leu	Glu	Asp	Gly	Arg	Ser	Glu	Thr	Val	Asp	Cys
	245					250						255			
Leu	Ile	Trp	Ala	Ile	Gly	Arg	Glu	Pro	Ala	Asn	Asp	Asn	Ile	Asn	Leu
	260					265					270				
Glu	Ala	Ala	Gly	Val	Lys	Thr	Asn	Glu	Lys	Gly	Tyr	Ile	Val	Val	Asp
	275					280					285				
Lys	Tyr	Gln	Asn	Thr	Asn	Ile	Glu	Gly	Ile	Tyr	Ala	Val	Gly	Asp	Asn
	290					295					300				
Thr	Gly	Ala	Val	Glu	Leu	Thr	Pro	Val	Ala	Val	Ala	Ala	Gly	Arg	Arg
	305					310				315			320		

Leu Ser Glu Arg Leu Phe Asn Asn Lys Pro Asp Glu His Leu Asp Tyr
 325 330 335
 Ser Asn Ile Pro Thr Val Val Phe Ser His Pro Pro Ile Gly Thr Val
 340 345 350
 Gly Leu Thr Glu Pro Gln Ala Arg Glu Gln Tyr Gly Asp Asp Gln Val
 355 360 365
 Lys Val Tyr Lys Ser Ser Phe Thr Ala Met Tyr Thr Ala Val Thr Thr
 370 375 380
 His Arg Gln Pro Cys Arg Met Lys Leu Val Cys Val Gly Ser Glu Glu
 385 390 395 400
 Lys Ile Val Gly Ile His Gly Ile Gly Phe Gly Met Asp Glu Met Leu
 405 410 415
 Gln Gly Phe Ala Val Ala Leu Lys Met Gly Ala Thr Lys Lys Asp Phe
 420 425 430
 Asp Asn Thr Val Ala Ile His Pro Thr Ala Ala Glu Glu Phe Val Thr
 435 440 445
 Met Arg
 450

<210> 399
 <211> 2904
 <212> RNA
 <213> E. Coli

<400> 399

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cccgccuau	caacgucguc	gucuucaacg	uuccuucagg	acccuuuaag	ggucagggag	120
aacucaucuc	ggggcaaguu	ucgugcuuag	augcuuucag	cacuuauucuc	uuccgcauuu	180
agcuaccggg	cagugccauu	ggcaugacaa	cccgaacacc	agugaugcgu	ccacuccggu	240
ccucucguac	uaggagcagc	ccccucagu	ucuccagcgc	ccacggcaga	uagggaccga	300
acugucucac	gacguucuua	acccagcucg	cguaccacuu	aaaauggcga	acagccauac	360
ccuugggacc	uacuucagcc	ccaggaugug	augagccgac	aucgaggugc	caaacaccgc	420
cgucgauaung	aacucuuggg	cgguaucagc	cuguuauccc	cggaguaccu	uuuauccguu	480
gagcgauggc	ccuuccauuc	agaaccaccc	gaucacuaug	accugcuiuc	gcaccugcuc	540
gcgcgcucac	gcucgcaguc	aagcuggguu	augccauugc	acuaaccucc	ugauguccga	600
ccaggauuag	ccaaccuucg	ugcuccuccg	uuacucuuua	ggaggagacc	gccccaguca	660
aacuaccac	cagacacugu	ccgcaacccg	gauuacgggu	caacguuaga	acaucaaaca	720
uuuaagggug	guauuuucaag	gucggcucca	ugcagacugg	cguccacacu	ucaaagccuc	780
ccaccuaucc	uacacaucaa	ggcucaaugh	ucagugucaa	gcuauaguua	agguucacgg	840
ggucuuuccg	ucuugccgcg	gguacacugc	aucuucacag	cguuuuacau	uucacugagu	900
cucgggugga	gacagccugg	ccaucauac	gccaucgcug	caggucggaa	cuuacccgac	960
aaggaauuuc	gcuaccuuag	gaccguuaua	guuacggccg	ccguuuuaccc	ggccuucgau	1020
caagagcnuuc	gcuugcgcua	accccaucaa	uuuaccuuuc	ggcacccggc	aggcgcucaca	1080
ccguauacgu	ccacuuucgu	guuugcacag	ugcuguguuu	uuauuaaaca	guugcagcca	1140
gcugguaucu	ucgacugauu	ucagcuuccau	ccgcgaggga	ccucaccuac	auaucagcgu	1200
gcciuucuccc	gaaguuacgg	caccauuuug	ccuaguuccu	ucacccgagu	ucucucaagc	1260
gccuugguau	ucucuaccug	accaccugug	ucgguuuggg	guacgauuug	auguuaccug	1320
augcuuagag	gcuuuuccug	gaagcaggcc	auuuguugc	ucagcaccgu	agugccucgu	1380
caucacgccc	cagccuugau	uuuuccggauu	ugccuggaaa	accagccuac	acgcuuuaac	1440
cgggacaacc	gucgcccggc	caacauagcc	uucuccgucc	ccccuucgca	guaacaccaa	1500
guacagggaaau	auuaaccugu	uucccaucga	cuacgccuuuu	cggccucgccc	uuaggggucg	1560
acucacccug	ccccgauuua	cguuggacag	gaaccuuugg	ucuuccggcg	agcggccuuu	1620
ucacccgcuu	uaucguuacu	uaugucagca	uucgcacuuc	ugauaccucc	agcaugccuc	1680
acagcacacc	uucgcaggcu	uacagaacgc	uccccuaccc	aacaacgcau	aagcgcucgcu	1740
gccgcagcuu	cggugcaugg	uuuagccccg	uuacaucuuuc	cgcgcaggcc	gacucgacca	1800

gugagcuauu acgcuuucuu uaaaugaugg cugcuucuaa gccaacaucc uggcugucug	1860
ggccuuuccca caucguuuucc cacuuaacca ugacuuuuggg accuuagcug gcgucuggg	1920
uuguuuuccu cuucacgacg gacguuagca cccgccgugu gucuccgug auaacauucu	1980
ccgguaauucg caguuugcau cggguuggua agucgggaug acccccuiugc cgaaacagug	2040
cucuaccccc ggagaugaau ucacgaggcg cuaccuaaaau agcuiuucggg gagaaccagc	2100
uaucucccg uuugauuggc cuuucacccc cagccacaag ucauccgcua auuuuucaac	2160
auuagucggu ucgguccucc aguuuagugu acccaacuu caaccugccc auggcuagau	2220
caccggguuu cgggcuuaua cccugcaacu uaacgcccag uuaagacucg guuuuccciuc	2280
ggcuccccua uucgguaaac cuugcuacag aauauaaguc gcugacccau uauacaaaag	2340
guacgcaguc acacgcuuaa gcgugcuccc acugcuugua cguacacggu uucagguucu	2400
uuuucacucc ccucgccggg guucuuuucg ccuuuuccuc acgguacugg uucacuaucg	2460
guacgucagg aguaunuugc cuuggaggau ggucccccua uauucagaca ggauaccacg	2520
ugucccgccc uacucaucga gcucacagca ugugcauuu uguguacggg gcugucaccc	2580
uguaucgcgc gccuuuccag acgcuuuccac uaacacacac acugauucag gcucugggcu	2640
gcucccccguu cgcucgccgc uacuggggga aucucgguug auuuucuuuuc cucggguac	2700
uuagauguuu caguuccccc ggiucgcccuc auuaaccuaau ggauucaguu aaugauagug	2760
ugucgaaaca cacuggguuu ccccauucgg aaaucgcccgg uuauaacggu ucauaucacc	2820
uuaccgacgc uuauucgcaga uuagcacguc cuucaucgccc ucugacugcc agggcaucca	2880
ccguguacgc uuagucgcuu aacc	2904

<210> 400
<211> 120
<212> RNA
<213> E. Coli

<400> 400

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guuucacuuc ugaguucggc auggggucag gugggaccac cgccuacggc ccgcccaggca	120

<210> 401
<211> 76
<212> RNA
<213> E. Coli

<400> 401

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ccccuagggg acgcca	76

<210> 402
<211> 1549
<212> RNA
<213> E. Coli

<400> 402

aaauggaaga guuugaucau ggcucagauu gaacgcuggc ggcaggccua acacaugcaa	60
gucgaacggu aacaggaagc agcuugcugc uucgcugacg aguggcgac gggugaguaa	120
ugucugggaa gcugccugau ggagggggau aacuacugga aacgguacgu aauacccgcau	180
aauugucgaa gaccaaagag ggggaccuuic gggccucuug ccaucgggaug ugcccagaaug	240
ggauuagcuu guuggugggg uaacggcuca ccaaggcgac gaucccuacg ugguucugaga	300
ggaugaccag ccacacugga acugagacac gguccagacu ccaucgggag gcagcagugg	360
ggaauauugc acaaugggcg caagccugau gcagccaugc cgcguguaua aagaaggccu	420

ucggguugua	aaguacuuuc	agcggggagg	aaggagauaa	aguuaauacc	uuugcuauu	480
gacguuaccc	gcagaagaag	caccggcuu	cuccgugcca	gcagccgcgg	uaauacggag	540
ggugcaagcg	uuauucggaa	uuacugggcg	uaaagcgcac	gcaggcgggu	ugguuuaguc	600
agaugugaaa	uccccgggcu	caaccuggga	acugcaucug	auacuggcaa	gcuugagucu	660
cguagaggggg	gguagaauuc	cagguguagc	ggugaaaugc	guagagauu	ggaggaauac	720
cgguggcgaa	ggcggcccc	uggacgaaga	cugacgcuca	ggugcgaaag	cguggggagc	780
aaacaggauu	agauacccug	guaguccacq	ccguuaacga	ugucgacuug	gagguugugc	840
ccuugaggcg	uggcuuccgg	agcuaacgcg	uuaagucgac	cgccuggggg	guacggccgc	900
aagguaaaaa	cucaaaugaa	uugacggggg	cccgcacaag	cgguggagca	ugugguuuaa	960
uucgaugcaa	cgcgaagaac	cuuaccuggu	cuugacaucc	acggaaguuu	ucagagaua	1020
gaaugugccu	ucgggaaccg	ugagacagg	gcugcauggc	ugucgucagc	ucguguugug	1080
aaauguuggg	uuaagucccg	caacgagcgc	aaccuuuac	cuuuguugcc	agcgguccgg	1140
ccgggaacuc	aaaggagacu	gccagugaua	aacuggagga	agguggggau	gacgucaagu	1200
caucauggcc	cuuacgacca	gggcuacaca	cgugcuacaa	uggcgcauac	aaagagaagc	1260
gaccucgcga	gagcaagcgg	accucauaaa	gugcgcugua	guccggauug	gagucugcaa	1320
cucgacucca	ugaagucgga	aucgcuagua	aucguggauc	agaaugccac	ggugaaauacg	1380
uucccgcc	uuguacacac	cgcccgcucac	accaugggag	uggguugcaa	aagaaguagg	1440
uagcuaacc	uucggggaggg	cgcuuaccac	uuugugauuc	augacugggg	ugaagucgua	1500
acaagguaac	cguaggggaa	ccugcgguug	gaucaccucc	uuaccuuuaa		1549

<210> 403
<211> 17
<212> DNA
<213> Artificial

<220>
<223> Primer Oligonucleotide

<400> 403

tgtttatcag accgctt 17

<210> 404
<211> 18
<212> DNA
<213> Artificial

<220>
<223> Primer Oligonucleotide

<400> 404

acaatttcac acagcctc 18

<210> 405
<211> 159
<212> DNA
<213> Escherichia coli

<400> 405

cagggttat ggaaacctaa aatggagacg ggaagctgaa ccagatagtt actggagggtg 60
atcaccagca gatgaaataa cgataaccag aacaacgcct tatagcgttg agttgcgag 120
aaaacgttca tattgtacct tttgattaa ccattgggg 159

<210> 406

<211> 640

<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(640)
<223> n = A,T,C or G

<400> 406

gggnccaaa	gtgtttgggn	cgggcaactg	gaggccaacc	ttaantnng	ggaaattttt	60
aanaaaaggc	ggggatttgt	nagccacggg	ngattanttt	anaataaaatt	aagtttgcc	120
ataaggggac	aaagngaagg	aagtggntat	taangannc	gccaatgcga	nttagggcag	180
accattcggc	cattcgctt	cttggttate	gaagttcatc	cagatagccg	ttgcngacc	240
gaccagattc	gcttcnggca	caaagccccca	gtaacggctg	tccgcgctgt	tgtcgcggtt	300
gtcgcccattc	atgaagtatt	gtcccgagg	aacaatccag	tttgccagtt	tttgcctgg	360
ctgctggtaa	tacatcccc	cctgatcctg	cgcaatcgcc	actgtcagaa	tgcggtgcgt	420
cacatcaccc	agtgtcttt	tacgctcgga	aagacgaatt	ccatttctt	tggtttcgtt	480
tttcggact	tcaaagaatc	cgtggtcgc	ttcccccacca	ttacggcgtg	agaaggtctg	540
aacaaatcg	ctcggttcca	cgtttgagta	ggtgaccggc	agcgcgtttt	cacacgcctg	600
ccggaaactg	catcccggtt	aatcgtcag	ctctttttag	.	.	640

<210> 407
<211> 682
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(682)
<223> n = A,T,C or G

<400> 407

cctgcagggt	aatgtcgcca	ttaaactggc	gcaggcagcc	aaagagttgc	tccgcttcta	60
cccagtccgc	agcgacaact	tgcgttaaag	tcgaaaatt	atcatctgca	ctcaactgcgt	120
gacgtaagcg	gatggagtgg	ccggaaacct	catagtgacc	gccaccagt	tggctgcat	180
cgtttgttag	cgtacgcgcg	gcattggcaa	taagatttag	atactcagac	tcttcgggg	240
ccttcggccag	cataaaagag	gaggatgctc	gcgtatgcag	caactgctcc	agcgcaatt	300
gcagccgcgg	ttgagtatca	ctgaataaag	gatcgtttc	gtcaatcaa	tgtggctgag	360
caaatatttc	ctgatagcta	tcggatcag	gaaccaggc	acgccatgca	agtttgcata	420
tggtaaagt	tgtgttttt	tagtctgtt	tcaaagccgc	nattataccn	gtaacccgca	480
ctacagcaca	cgtagaaagc	acccgacaat	actcctggca	tggcgttaa	agctcacagg	540
atggagatct	tttcttact	ggcctaaaaa	gctgatattc	tgtaaagagt	tacacngtaa	600
catttagatc	gctatgaaat	atcaacaact	tggaaaatct	tgnaaagcng	gttggaaaat	660
ggaaagtatc	tggtaagaa	gc	.	.	.	682

<210> 408
<211> 309
<212> DNA
<213> Escherichia coli

<400> 408

gggatccgg	cagaatttta	cgctgaccaa	tgacgcgacg	acgtggcatg	gaaatactcc	60
gttgttaatt	caggattgtc	caaaactcta	cgagttagt	ttgacattt	agttaaaacg	120
tttggcctta	cttaacggag	aaccattaag	ccttaggacg	cttcacgcca	tacttggAAC	180
gaggctgctt	acggcttta	acgcccggagc	agtcaagcgc	accacgtacg	gtgtggtaac	240
gaacacccgg	gaggtcttta	acacgaccgc	cacggatcag	gatcacggag	tgctcctgca	300
ccaaagctt	309

<210> 409
<211> 1167
<212> DNA
<213> Escherichia coli

<400> 409

gtcgacccat	ctgtccattg	agcggacagt	tttgtcaaca	ctatTTGTT	gaccggaaaa	60
tggAACACTT	tccgcaatgc	ctgttgctat	cacgcttaaa	ccatttcatt	gcgatttaca	120
cagaacggac	gtcctgtcgc	agtatattaa	gtcgtcgata	gaaacaagca	ttgaaaggca	180
cagcagtagt	caaacagtgt	gaaacgctac	tggcgcccta	cagcgcaaaa	aggctggtga	240
ctaaaaagtc	accagccatc	agcctgattt	ctcaggctgc	aaccggaaagg	gttggcttat	300
ttaacttcaa	ttcagcgcgc	agettcttcc	agagctttt	tcagtgcTTT	tgcgtcgct	360
ttgctcacgc	cttctttcag	agcagccgg	gcagattcta	ccaggtctt	agcttcttc	420
agacccaggc	cagttgcgc	acgtactgct	ttgataaacag	caacttgg	agcgccagca	480
gcttcagaa	ttacgtcgaa	ttcagttttt	tcttcagcag	cttcaaccgg	gccagcagct	540
acagctacag	cagcagcagc	ggaaaacaccg	aatttttctt	ycattgcaga	gatcaagttc	600
tacaacgtcc	attacagaca	tagctgcaac	tgcttcaatg	awttgatctt	tagtgcata	660
catttaatk	gttcctgaat	atcagaataa	gtttatacgt	aagcgaatgc	gttaaaaaga	720
taactgcgaw	taagcagctt	ytttcgcatac	gcgtacagma	gccagagtac	gaaccagttt	780
gccagccgaa	gcttcttca	tggttgccat	caggcgtgca	attgcttctt	cgtaggtcgg	840
cagagttgcc	aggcgggtcga	tctgagacgc	cgggatcagc	tcaccttcaa	aggcagccgc	900
tttgcacctca	aattttgcata	tcgcttgcgc	gaactcttt	aacagacgag	cagcagccgc	960
cgggtgttcc	atagagtagt	caatcagggt	cggaccaca	aacgcgtctt	tcaggcactc	1020
gaacggagta	ccttcaacag	cacggcgcag	cagggtgtta	cgaacaacac	gcatgtatac	1080
gccagcttcg	cgacctgctt	tacgcagttc	agtcatTTT	tctacagttt	cggccacggg	1140
aatccgcaac	tactgcaagc	caagtt				1167

<210> 410
<211> 404
<212> DNA
<213> Escherichia coli

<400> 410

caacmctatt	ttgktggacc	ggaaaakgga	acactttccg	cawkgcctgt	tgctatcacg	60
cttaaaccat	ttcattgcga	tttacacaga	acggacgtcc	tgtcgcgat	tattaagtcg	120
tcgatagaaa	caagcattga	aaggcacagc	agtatcAAA	cagtgtgaaa	cgctactggc	180
gccttacagc	gcaaaaaggc	tggtgactaa	aaagtccacca	gccccatcagcc	tgatttctca	240
ggctgcaacc	ggaagggtt	gcttattaa	cttcaacttc	agcgccagct	tcttcagag	300
ctttttcag	tgcttctgcg	tgcgtttgc	tcacgcctc	tttcagagca	gccgggtgcag	360
attctaccag	gtcttagct	tcttcagac	ccaggccagt	tgcg		404

<210> 411
<211> 152
<212> DNA
<213> Escherichia coli

<400> 411

agagctttt	tcagtgcTTT	tgcgtcgct	ttgctcacgc	cttctttcaa	gagcagcccg	60
gtgcagattc	taccaggct	ttagcttctt	tcagacccag	gccagttgcg	ccacgtactg	120
ctttgataac	agcaacttt	ttagcgc	ca			152

<210> 412
<211> 825
<212> DNA
<213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(825)
 <223> n = A,T,C or G

<400> 412

gatccgtcga	cccatctgtc	cattgagcg	acagtttg	caacactatt	ttgttgaccg	60
gaaaatggaa	cacttccgc	aatgcctgtt	gctatcacgc	ttaamccatt	tcattgcgt	120
ttacacagaa	cgjacgtcct	gtcgcagtat	attaagtcgt	cgatagaaac	aaggattgaa	180
aggcacagca	gtagtcaa	agtgtgaaac	gctactggcg	cttacagcg	caaaaaggct	240
ggtgactaaa	aagtcc	ccatcagcct	gatttctcag	gctgcaaccg	gaagggttgg	300
cttatttaac	ttcaactca	gcccagc	cttccagagc	ttttttagt	gttctgcgt	360
cgtcttgc	cacgc	ttcagagcag	ccgggtgcag	attctaccag	gtcttagct	420
tcttcagac	ccaggcc	tgccacgt	actgcttga	taacagcaac	ttttagcg	480
ccagcagctt	tcagaattac	gtcgaattca	agtttttct	ttagcagctt	caaccggcc	540
agcagctaca	gctacagcag	cagcagcg	aacaccgaat	ttttcttyca	ttggcagaga	600
tcaagttcta	caacgtccat	tacagacata	gctgcaactg	cttcaatgat	tkgatcttw	660
gtgatagaca	tttaaattgt	tcctgaatat	cagaataagt	ttatacgtaa	gcgaatgcgt	720
taaaaagata	actgcgatta	agcagcttct	ttcgcatcg	gtacagcagc	cagaggtcga	780
accagttgc	cagccgaagg	ttggctttc	agcctnnncn	natta		825

<210> 413
 <211> 425
 <212> DNA
 <213> Escherichia coli

<400> 413

agtagtcaa	caggtgkgra	acgctactgg	cgccttacag	cgcaaaaagg	ctgggtacta	60
aaaagtca	agccatarc	ctgatttctc	aggctgcaac	ccggaaagggt	tggcttattt	120
aacttca	acttcact	tcagcgccag	cttcttccag	agcttttctc	agtgc	180
gctcacgc	ctttcagag	cagccggtgc	agattctacc	aggtctttag	cttctttag	240
accaggc	gttgc	ccacgt	acttgc	gataacagca	acttgc	300
tttcagaatt	acgtcgaatt	cagtttttc	ttcagcagct	tcaaccggc	cagcagctac	360
agctacagca	gcagcagcgg	aaacaccga	attttctc	cattgcagag	atcaagttct	420
acaac						425

<210> 414
 <211> 126
 <212> DNA
 <213> Escherichia coli

<400> 414

agagctttt	tca	tcgtcg	tgcgtct	ttgctcacgc	cttctttag	agcagccggt	60
gcagattcta	ccagg	ttt	agcttctt	agacc	cagg	tgccgc	120
ttrata						acgtactgct	126

<210> 415
 <211> 264
 <212> DNA
 <213> Escherichia coli

<400> 415

ctgcma	ccccg	garggg	ttgg	cttatttaac	ttcaactca	gcccagc	tttgcag	60
tttttca	ag	tgcttctgc	tcgtcttgc	tcacgc	cttc	agc	gccc	120
atttacc	ag	gtctttag	ctttcagac	ccaggcc	actgc	tttgc	actgc	180
taacagca	ac	tttgc	ccagcag	tttgc	tcagaatt	gtcgaatt	tttttctt	240
cagcag	ttc	ccagcag	tttgc	tttgc	gttgc	tttgc	tttgc	264
aaccgg	cca	ccagcag	tttgc	tttgc	tttgc	tttgc	tttgc	
gcag								

<210> 416
 <211> 201
 <212> DNA
 <213> Escherichia coli

<400> 416

cgcataccct	gcagcatcg	cccgatggag	atcaggtcgg	cagaacgctg	taccgcttg	60
tagtgtgt	taccgggtt	cagatccgg	aagatgaaca	cggttagcgcg	acctgcaacc	120
ggagagttcg	gchgcttgga	tttcgcaacg	tcagccatta	ccgcagcgtc	gtactgcagc	180
ggaccgtcga	tcatcaggtc	a				201

<210> 417
 <211> 239
 <212> DNA
 <213> Escherichia coli

<400> 417

aattcagcag	ttgacagtgg	cataaacgta	actggtgact	tttgcggcgc	atgacgcgg	60
gctttttta	ttattccgtg	acttccagcg	tagtgaaggc	aaacttctcg	ccatcaaata	120
gcccctgact	ggttagttt	agcgcgggga	tcactggcag	agaaagaaaac	gccatctgaa	180
taaacggctc	atcgggtaac	ggaccgcatt	cacggcggc	ggcttcaag	gcgtcaatt	239

<210> 418
 <211> 223
 <212> DNA
 <213> Escherichia coli

<400> 418

ttctttttt	cgtcaacgg	gtccagaatc	attttattta	cctcggtac	ttatgctgat	60
tttttatttt	atggggaaagg	tgttatttt	gagtttcatt	tatgccgtaa	cgacaatgaa	120
ctcgggaatt	agtataagca	gchgagaaat	aataatcatt	gtgcaaatgc	taatttaatt	180
aatactattt	aaatattatt	ttgagcatat	gcacataagg	ttt		223

<210> 419
 <211> 223
 <212> DNA
 <213> Escherichia coli

<400> 419

ttctttttt	cgtcaacgg	gtccagaatc	attttattta	cctcggtac	ttatgctgat	60
tttttatttt	atggggaaagg	tgttatttt	gagtttcatt	tatgccgtaa	cgacaatgaa	120
ctcgggaatt	agtataagca	gchgagaaat	aataatcatt	gtgcaaatgc	taatttaatt	180
aatactattt	aaatattatt	ttgagcatat	gcacataagg	ttt		223

<210> 420
 <211> 212
 <212> DNA
 <213> Escherichia coli

<400> 420

aatagcgggt	atgcacgcct	ttctttttt	cgtcaacgg	gtccagaatc	attttattta	60
cctcggtac	ttatgctgat	tttttatttt	atggggaaagg	tgttatttt	gagtttcatt	120
tatgccgtaa	cgmcaatgaa	ctcgggaatt	agtataagca	gchgagaaat	aataatcatt	180
gtgcaaatgc	taatttaatt	aaatactattt	aa			212

<210> 421

<211> 438
 <212> DNA
 <213> Escherichia coli

<400> 421
 ccctgtaaat tatcgccgtt ggataaaaaa ctgcgtccaa acgcccgtt tgccagc
 caggccataa atgccaccag aattatcgta aaccaaccaa ttgctgaaac gccaagc
 agcggggcgg agagctgtt cagttcgccg ggttaaccctt caatccattt gccgccc
 cacagcaaca ttagtcctt gtacaaccctt aacgtgccaa gggtgttgcac aatggc
 atcttttagcc acgcgaccag gacaccgtt aaaaatccc cgagcaaacc aagc
 gtcgcacac aagcaacagg tagtgaatat cctgcgttca gtaacatccc caacagc
 gcgacattt cggtaatcg aacccactt gaaacatcaa tattgsqsgt aagcattwcc
 aagcgttcgs gccccatkg 438

<210> 422
 <211> 682
 <212> DNA
 <213> Escherichia coli

<400> 422
 aattcccggtt gatccgtcga ccgtgcgtt ccgggttggg caacccgcga aatggc
 cggtaagtat ggccgggtta ttccctccccc gttgaggaca ccgggttgc aggtt
 tacgcttaag tgacaacccc gctgcaacgc cctctgttat caatttctg gtgac
 gcggtatcg ttttactccg tgactgctt gcccgcctt ttaaagtgaa ttttgatg
 tggtaatgc ggctgagcgc acgcgaaaca gttaaaacca aaaacagtgt tatgg
 ttctctgtat ccggcgtaa ttgttaactg gttaacgtca cctggaggca ccagg
 catcacaaaaa ttcatgttg aggacgcgtt aatgaaaacg ttattaccaa acgtt
 gtctgaaggt tgaaaaaaa ttgggtgtcac tattacaa ccaacttta ctga
 cattaacaag agaaaaacaag aacgggagct attaaataaa atatgcattt ttt
 ggctcggtt cgtctgtatgc caaaaaggatg tgcacaatga attcagcatt ttt
 ctgacagttt ttctgttcc cggagagcca gttgatattt cagtcgtgt tcacagg
 atgcaggagt gatgactgca gc 682

<210> 423
 <211> 600
 <212> DNA
 <213> Escherichia coli

<400> 423
 ggggatccga ttgtgactgc tctgccccc ttttaaagt gaattttgtg atgtgg
 tgcggcttag cgacgcgga acagttaaa ccaaaaacag ttttatggg ggattct
 tatccggcgt taattgttaa ctggtaacg tcacctggag gcaccaggca ctgc
 aaattcattt ttgaggacgc gataatgaaa acgttattac caaacgttac tac
 gtttttttgg aaattgggtt cactatcgtt aacccagtat ttactgaaga tgcc
 aagagaaaaac aagaacggga gctattaaat aaaatatgca ttgttcaat gct
 ttacgtctga tgccaaaagg atgtgcacaa tgaattcagc atttgcattt gtt
 ttttcttgc ttccggagag ccagttgata ttgcagtcg tttcacagg acaat
 agtgcacatgc tgcagcaacc gaacagaaaa ttcccgtaa ctgttaccc gtc
 ttattcacca ggataatatc gaaatccgg caggtcttta aacagttccg taata
 600

<210> 424
 <211> 100
 <212> DNA
 <213> Escherichia coli

<400> 424
 gggatccagc aagaagatgc gtttgcgttccg tcatcacgca gatgcgcaaa gct
 tactcagc 60

aactgacctt	tcttcgaat	aagcacgcca	ttagcgtcat	100		
<210>	425					
<211>	465					
<212>	DNA					
<213>	Escherichia coli					
<400>	425					
tcgcgtgttt	accttcaaca	tcggtaactt	tctggcgat	agtttcacgg	taagcaacct	60
gcggtttacc	tacgttcgct	tcaacgttga	attcacgctt	catacggtca	acgatgtatgt	120
cgaggtgcag	ttcgccata	cccgcgatga	tggtctggtt	agattcttcg	tcagtccata	180
cacggaaaga	cgggtttct	ttagccagac	ggcccagagc	cagaccattt	ttttcctgg	240
cagcttttgtt	tttcggttca	actgcgtatgg	agattaccgg	ctcaggaaat	tccatacgtt	300
ccagaatgtat	cggcgcatcc	gggtcacaca	gggtgtcacc	agtggttacg	tcttcagac	360
cgtatgcgc	agcgatgtcg	cccgcgcgaa	cttcttgat	ctcttcacgt	ttgttagcgt	420
gcatactgaac	gatacgcaccg	aaacgctcac	gtgcagctt	cacgg		465
<210>	426					
<211>	653					
<212>	DNA					
<213>	Escherichia coli					
<220>						
<221>	misc_feature					
<222>	(1)...(653)					
<223>	n = A,T,C or G					
<400>	426					
tgatcggctc	aagcagaact	ggtttcgctt	tcttaaagcc	ttctttaaag	gcgatagaag	60
cagccagttt	aaacgcccagt	tcagaggagt	caacgtcatg	gtaagaaccc	aagtgcagac	120
gaataccat	gtctactacc	gggttagcctg	ccagcgacc	tgctttcagc	tgttcctgg	180
tacctttatc	aacggccggg	atgtattcgc	cagggattac	accaccttta	atgtcgttga	240
tgaactcgta	gcctttcggg	tttgaaccccg	gctccagcg	gtacatgtcg	ataacaacat	300
gaccatactg	accacgacca	ccagactgtt	tcgcgtgttt	accttcaaca	tcggtaactt	360
tctggcgat	agtttcacgg	taagcaacct	gccccttacc	tcgatcgct	tcaacgttga	420
attcacgctt	catacggtca	acgtatgtgt	cgaggtgcag	ttcgccatac	cccgcatgtat	480
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gccagagnca	gaccattttt	tttctggcag	cttggnttc	ggtaactgc	gatggaaata	600
ccggctcaa	ggaattcata	cgttcanaa	tgatcgggc	attccgggtc	aca	653
<210>	427					
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<212>	DNA					
<213>	Escherichia coli					
<400>	427					
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agtcaacgtc	atggtaagaa	ccgaagtgc	gacgaatacc	catgtctact	accgggtac	120
ctgcccagcg	acctgtttc	agctgttct	ggataccctt	atcaacggcc	gggatgtatt	180
cccgaggat	tacaccacct	ttaatgtcgt	tgtactc	gtagccttc	gggttgaac	240
ccggctccag	cggtacatg	tcgataaac				268
<210>	428					
<211>	330					
<212>	DNA					
<213>	Escherichia coli					

<400> 428		
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atgactgatt gccgataacct gattaaacgg gtcataaaa tcatacattgc tgtttacag	120	
ctgatccttc tgttctata acacaaggaa acgtactaa ggtcggtccg gtgaaccagt	180	
cggacgcacc ttataact ataaataagt gtctggcag atactatata aattaactta	240	
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aatataatta atactctact tccagagtag	330	
<210> 429		
<211> 465		
<212> DNA		
<213> Escherichia coli		
<400> 429		
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atgactgatt gccgataacct gattaaacgg gtcataaaa tcatacattgc tgtttacag	120	
ctgatccttc tgttctata acacaaggaa acgtactaa ggtcggtccg gtgaaccagt	180	
cggacgcacc ttataact ataaataagt gtctggcag atactatata aattaactta	240	
gtaatgatt atgctaatgt catcaattaa ataaatataa tggcgtaag gcttcccagt	300	
aatataatta atactctact tccagagtag aatattaaat ttatcccg tggcatca	360	
gcacaaattt atcccacaac tgttcttctg tctcgacatg cgccggatct ttcacaatag	420	
tattgggat cggcacacc ttctggcagg ttgggtctc gtatg	465	
<210> 430		
<211> 379		
<212> DNA		
<213> Escherichia coli		
<400> 430		
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ttaaacgggt catcaaaatc atcattgctg tttacagct gatccttctg ttcttataac	120	
acaaggaaac gtacttaagg tgcgtccggtaa acccaggatcg gacgcaccc taataactat	180	
aaataagtgt ctggcgat actatataaa ttaacttagt gaatgattat gctaatgtca	240	
tcaattaaat aaatataatg gcgttaaggc ttcccagtaa tataattat actctacttc	300	
cagatgaa tattaaat ttatcccg tgcacatgc acaaatttat cccacaactg	360	
ttcttctgtc tcgacatgc	379	
<210> 431		
<211> 443		
<212> DNA		
<213> Escherichia coli		
<400> 431		
aagatgtatg gatgagaaag tcaatttgaat taagacaata ttaagagcta aaaaaatgtc	60	
aaaaaacact aaatcaaaaa ataatggcat tagaaaaat aatgcggaaa cggagggtgaa	120	
attatgttat ttcaaatgag gaaaatctcc cggcgaaaa accggggat gaaagtgtga	180	
tgggtatcaa ataaacaaca gaggagaaat tttaacgcgca gccattcagg caaatcgaa	240	
aatcccatttgc cctggcgat aagttgcggc ttaacgccag gaagcgtgtc ggccagttc	300	
aaaccaatatac cacgcacccat tttttcgcc ggattggtac cggaaaaacag atcgccaaat	360	
ccctgcatac cagccacat caacgcgcga ctgtgcttgc ggctacgc atagcgacgc	420	
agataaatgt actgccccat gtc	443	
<210> 432		
<211> 638		
<212> DNA		
<213> Escherichia coli		

<400> 432		
cagggggttt gttgtggca atgatgcatt taagtatcg tctgcagata gaggagatat	60	
tacaataaac aacgaatcag ggcatttgat agtcaatacc gcaattctat caggagatat	120	
agtcaactcta agaggaggag aaatttagtt ggtattatag cttgtgcgcg ccatgattgg	180	
cgcgcattt aaacttagtgc ttacatcg ctattgtctt gatttctt aattatcca	240	
taaattaaaaaa aaacgactgt tatgtataag caaagtccg aacgaaaaat acattccaaa	300	
taaatgcctg cttaaatctc tatatccttc cccgaaaaat gacacataaa attgagatat	360	
tccaaaaaga gatactacaa ataaagatgc cttaatttta ttatctaa taaaaataga	420	
agcaataaaaaa aataataaca atgatataaa tctaattttt ttaaatataat tgcattttat	480	
gttagtaata gtcgttagta tggtttagttccatataatt acgtgttagttttatatac	540	
atgaaataaa ttttctttat actgagacat cacaccatca tcaaattggaa gtttgaagat	600	
ggtgcttgggtt gcttaacca ataaaaagag tgcattcg	638	
<210> 433		
<211> 299		
<212> DNA		
<213> Escherichia coli		
<400> 433		
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acagaatgcc cattgttcc tcacttatct gtttgcatt agcgggttag tcgctgataa	120	
aaagcatagc acaacatcg gaggcaaga tttgtacga gcatcacgga ggttttttg	180	
cgatggcgca gaaattgcgc catcaacgat cagtataat taccaccac aaacatcatg	240	
ttcggtttcc gtgtcataag aacgtacggg attcaccaga tttttatca cttcagccg	299	
<210> 434		
<211> 388		
<212> DNA		
<213> Escherichia coli		
<400> 434		
gaaaaaggag gcaatatcggtt gtaaaggcat tagccgcacg aatacgtcg gctacaata	60	
ttattgtgtc gcaggtgtt tagcggttg ttgatccaca gtttctaact ggaagaccac	120	
atcgacctga tcataacttgcgac ccgttttacg atgaaagccg ttgcgcatttgcgtt	180	
cgccgcattcg gcttcattca tccgcaccat tggctggc tgatagttgg aaacatggta	240	
gcccgcgttataccggcc ccagtttacg atgaaagccg ttgcgcatttgcgtt	300	
atgaaatcggtt ttagtataatcg ctgccttacg cgctttgtct ttataggcat ccggctgcgc	360	
caccccccacg gacacagaac gaattcccc	388	
<210> 435		
<211> 351		
<212> DNA		
<213> Escherichia coli		
<400> 435		
ctatccttgc taaaaccgcg agcaaagata ggtgattacg tcatggttt acagaaaaatt	60	
acagaaaaat gaggcaatat cgggtaaagg cattagcccg acgaatacgtt cgggcataaa	120	
atattattgt gctgcagggtt ttttagcggtt ttgttgcattt acaggttcta actgaaagac	180	
cacatcgacc tggatcatcaa actgaatagc ggcctgcgtt taagtttccctt gggcggacac	240	
cgccgcggca tcggctttca tcatccgcac cattggcgtt ggctgtatgt tggaaacatg	300	
gtagcgcacg ctatataccg gccccagttt acgtgaaag ccgttcgcac g	351	
<210> 436		
<211> 762		
<212> DNA		
<213> Escherichia coli		

<220>
 <221> misc_feature
 <222> (1)...(762)
 <223> n = A,T,C or G

<400> 436

aattatgaaa	cactgtctgg	aatcgctctga	atgacggca	catttgcag	cacgcata	60
gtaataaac	aggaaactat	tttatctacg	cgttagcgt	agactgcttg	catggc	120
ggaggtta	aggcgtt	agcgggacgc	tgaaacggg	aagccctcc	cgaggaagg	180
gccataaata	aggaaagggt	catgtgaag	ctactcatca	tcgtgg	tcttagtca	240
agcttccccg	cttactaaga	ctaccaggc	ggggaaaacc	ccgctctacc	ctcactcctg	300
aaagtatgcc	ttcacgataa	gattgtcaat	ccgcaggc	tgttagtctgc	gatcctgcca	360
gcaaata	tttgcgagtc	gttacgcaat	aatcacagag	gaaactattt	tattcacgcg	420
ttagcgtat	actgcattca	ggcgaaagg	aggtaagccg	atgatttc	cgggacgc	480
aaacggaaa	gcctctcc	gagaagagg	cttttaataa	gaaagggtt	atgatgaagc	540
acgtcatcat	actggtgata	ctcttagtga	ttagcttcca	ggcttactaa	gaacaccagg	600
gggagggg	aacctttcc	taaccctcac	ttctgaaatt	gggtgctatg	acgctggcgt	660
tactgcttan	cgctaccagt	ttgtctgccc	tggcggttgt	aacgccagat	cggtacc	720
ttgatattt	taatgaaagc	cgacaatca	atcancgtga	cg		762

<210> 437
 <211> 292
 <212> DNA
 <213> Escherichia coli

<400> 437

cacatttgcg	agcacgc	cagtaataac	acagggaaact	attttatcta	cgcgttagc	60
atagactgct	tgc	atggcga	aaggaggtaa	gccgacgatt	tcagcggac	120
gaaagccct	ccc	gaggaag	ggccataaa	taaggaaagg	gtcatgtga	180
catcggtg	ctcttagtca	taagcttccc	cgcttactaa	gactaccagg	gcggggaaa	240
ccccgc	ccctcactcc	tgaaagtatg	cctcacgat	aagattgtca	at	292

<210> 438
 <211> 631
 <212> DNA
 <213> Escherichia coli

<400> 438

atttacactt	tttacgaaat	catggatca	ctaacaaaat	atcgcttgc	agttatatt	60
tatggcagga	aagatatgc	actgatatta	cagatcccc	aagtggagag	tttatgacca	120
ttaaaaataa	gatgttgc	ggtgcgtt	tgctgg	tacgtccgc	tggccgcac	180
cagccaccgc	gggttcgacc	aatacctcg	gaatttctaa	gtatgagtt	agtagttca	240
ttgctgactt	taagcat	ttc	aaaccagg	acaccgtacc	agaaatgtac	300
agtacaacat	taagcagtgg	cagtgcgt	acctgcccgc	gcctgatgc	gggacgcact	360
ggacctat	gggtggcgc	ta	ctgtgttga	tcagc	gacac	420
cctacgacgg	tgagatttt	tatcatcg	aaaaaaagcc	ccctcatcat	gagggggaaa	480
tgcagacacc	ttgttattt	ttattattag	ccacttg	gtcttgctt	ttattagtc	540
tattcacgt	tgattaatgc	ggtgcctcc	agtgc	gccag	atthaactt	600
tagacgt	actggcgt	tatcg	aaattt	gtttgtatcg		631

<210> 439
 <211> 566
 <212> DNA
 <213> Escherichia coli

<400> 439

tatggcagga	aagatatgc	actgatatta	cagatcccc	aagtggagag	tttatgacca	60
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ttaaaaataa	gatgttgcgtg	ggtgtcgcttt	tgctggttac	cagtgccgcc	tggccgcac	120	
cagccaccgc	gggttcgacc	aatacctcg	gaatttctaa	gtatgagta	agtagttca	180	
ttgctgactt	taagcatttc	aaaccagggg	acaccgtacc	agaaatgtac	cgtaccgatg	240	
agtacaacat	taagcagtgg	cagttgcgt	acctgcccgc	gcctgatgcc	gggacgcact	300	
ggacctata	gggtggcg	tacgtgttga	tcagcgacac	cgacggtaaa	atcattaaag	360	
cctacgacgg	tgagat	tttatcgct	aaaaaaagcc	ccctcatcat	gagggggaaa	420	
tgca	gacacc	ttgttatttt	ttattattag	ccacttgctc	gtcttgctt	ttattatcg	480
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tagacgt	tagt	aactggctgt	atcgaa			566	
<210> 440							
<211> 339							
<212> DNA							
<213> Escherichia coli							
<400> 440							
cgtattcaca	tcctttgtat	tggtgataac	atgcgaatcg	gtattat	tccgggtt	60	
atcttcatta	cagcggcgt	attttagca	tggtttttta	ttggcg	gtctgc	120	
ggagcataaa	gatgaaaaaa	acaacgatta	ttatgatgg	tgtggcg	attgtcg	180	
tcggcactga	gctggatgg	tggtaacg	acctctaaa	aatagcaa	gctgc	240	
tgcagcctt	gtgcaattt	agcgtaact	ttttaatctt	ctgt	atagcac	300	
aatcgcacca	ataacggcaa	ccacgaagct	gccaaaatt			339	
<210> 441							
<211> 376							
<212> DNA							
<213> Escherichia coli							
<400> 441							
catgaatatt	taaaaaggaa	aacgacatga	aaccgaagca	cagaatcaac	attctccaat	60	
cataaaat	ttccgtggag	cattttatta	ttgaatata	aggtttaact	ccgtaaaaaa	120	
acaaagaagc	attgaatgca	gggaaaaata	atatggccat	aaaaaacatc	gaaagaaact	180	
cttttaattt	aacatgtaaa	cgcattt	atcctcatat	cacgggtt	gtgtt	240	
catacataaa	tggagtcat	ttttccctt	tccattt	aagttcctgt	tgccgtt	300	
gtccatctct	aattgcata	tttaattt	ctgataaaatg	gcattgagca	tcgattt	360	
ttaaaaacaac	tgtaca					376	
<210> 442							
<211> 446							
<212> DNA							
<213> Escherichia coli							
<400> 442							
ttacgatgc	tattgtaaa	aatataagag	ttagctgtat	tgttatgtct	gtggcgaaat	60	
tgactacctt	cgtttttt	attaagaatg	attttattat	cgttaagtaaa	attacatgaa	120	
tatttaaaa	ggaaaacgc	atgaaaccga	agcacagaat	caacattctc	caatcataaa	180	
atattccgt	ggagcattt	attattgaat	atagaggtt	aactccggt	aaaaacaaag	240	
aagcattgaa	tgcagg	aaaaatatgg	ccataaaaaa	catcgaaaga	aactcttta	300	
atthaacatg	taaacgc	gttaatcctc	atatcacggg	tggagtgtt	agaacataca	360	
taaatggagt	catgtt	tttccatt	tatcaagttc	ctgttgccgt	tttagtccat	420	
ctctaattgc	atatttaat	ttttct				446	
<210> 443							
<211> 388							
<212> DNA							
<213> Escherichia coli							

<220>
 <221> misc_feature
 <222> (1)...(388)
 <223> n = A,T,C or G

<400> 443

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ggaaaacaaa	gagataatg	tctaattcctg	atgcaaatcg	agccgatttt	ttaatcttta	120
cggactttta	cccgccctgg	tttattaattt	cactgnatc	ccccgcgttcg	cccgctttaa	180
tcacaatagg	ctgtgttagcc	tgggcctgtt	tctcttcac	ccgcgcaga	gcggcagcaa	240
tcgcacat	atctttggct	gcaggttga	cggctgcgt	tttatgtcgt	tcaaggcag	300
ccgccttttc	gcgctccaga	cgagctggc	gcgcttcgaa	acgcgccttg	gcttctgcgg	360
cncgcttttc	ttcctgacga	atagccgc				388

<210> 444
 <211> 209
 <212> DNA
 <213> Escherichia coli

<400> 444

aattttata	acgctatctg	cggataaaagc	agaatagggt	gttaacccca	gacataaacc	60
gagaaaaata	atgttattgt	atttcataat	ctattgttcc	ttagcgacag	attgctgtct	120
gctgggttcag	taaggttacca	ggagaaactt	caggaagctt	gtactcgaca	atacagttt	180
agttttatac	tttgccttcat	gaaacctgt				209

<210> 445
 <211> 341
 <212> DNA
 <213> Escherichia coli

<400> 445

catcctcaat	accgttaaat	gcaacccgaa	ccccgttgt	ccctttgctg	cattcactta	60
acgttatctg	aaaaggggacg	gctggacttg	tgctaccgt	cgttggaaat	tgtctggcac	120
tgttttttg	gagatctacg	gtaaaattaa	gcgaatccga	tgagactgtg	cagccataat	180
cgaggacgcg	cccgcttaatt	ttaataaacgc	tatctgcgga	taaagcagaa	tagttggta	240
accccagaca	taaaccgagg	aaaataatgt	tattgttattt	cataatctat	tgttccttag	300
cgacagattt	ctgtctgctg	gttcagtaag	gtaccaggag	a		341

<210> 446
 <211> 697
 <212> DNA
 <213> Escherichia coli

<400> 446

agatttactg	ccaatttccg	gcagatcgga	aagggttaam	ccatattgtat	ccataagggt	60
acgaatcmcg	ggctataccg	ccaggcatgg	cttgagccat	ggcattaaat	tccgcaaatt	120
cgggcgctga	ttcttcccac	gcggttattt	tggcacacac	cagatccagc	aagggttttt	180
caggatcggt	gagcagcaga	tgtatctacca	gttccagcgc	ctgggtgtat	tgttctctgt	240
tctgaatacc	cgccagaaaa	ggtgccacag	cagttagctt	ttctcctgt	tgcaagatgt	300
cggcaatcgc	aatcattttt	tccccttagt	acgatgaaca	gcggtaaaga	aatcgattt	360
tttatgcgtc	ataacttcac	gtatgttagca	cttttgcgt	tcaaaaaaaga	ccattgctac	420
aacacgtaat	tcattgcccc	caacattgaa	aacataatgc	ttatccagat	atttgaagtt	480
atccagagat	ggaaatactg	ctttaatga	ctcagggttt	ttgaaatatc	ccttagcaat	540
cgtgkcccc	agagccacca	actccgtttt	atgttgcggg	tattttccg	cagcatctt	600
caatgctttt	ttagttatca	ggtgcattct	tcatcacgtc	cgtkgmcaaa	ttggcaatat	660
gataacatcc	gttgcagat	ttgcacggat	gaattat			697

<210> 447
 <211> 215
 <212> DNA
 <213> Escherichia coli

<400> 447
 aattaataac ttttcgttag gcagtttgg gtgtgagttg caagagggga gactactgaa 60
 taactcaagt tttataatcg agggaaaat ggtgatggcg ttcatagcaa aacccccta 120
 accataaagg tcgagggcgc ttaagatgtt aaaaaccgc tatccgttaa aaaacaatgt 180
 tcaactaagg tcagtgacat tgcgctaaaa aagcg 215

<210> 448
 <211> 395
 <212> DNA
 <213> Escherichia coli

<400> 448
 gcattattca tgagaaatgt gtatcgtaaa tcaactgaaa ttaacgcaac catttgttat 60
 ttaaggtta attatctgtg tgtgatattt tattgaatgt tttaaatatt gtttttattg 120
 gcattgctat aatattgggtt atcatttgct gaatggattc agtcttaatg agtgggttt 180
 taagggacag gcatagagta atgatacgtt tgcataacca acatcttac tcattatgtc 240
 attgaatgtt gacgctatgt gtttatgagg gagaggtatt ttcaagttgat ctggattgtt 300
 aaattcatat aatgcgcctt tgctcatgaa tggatgccag tatgtatgtt gaaattataa 360
 atattgaaat agtccaacta cttcttattt accaa 395

<210> 449
 <211> 641
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(641)
 <223> n = A,T,C or G

<400> 449
 ataatcaggtaa aagaaaaggtaa ggcggagat taccgtgtgt tgcgatatat ttttttagttt 60
 cgcgtggcaaa tacatcagtgc acaataaaac gacatataccaa gaaaaatataa cactaagtga 120
 atgatatactt ccgattttatc ttaatcggtt atggataaacg gcaaaagggtt tcgtttttc 180
 ctatacttat tcagcactca caaataaaagg aacgc当地atgaaaattatac tctgggtgtt 240
 attgattatt ttccctgattt ggctactgtt ggtgactggc gtatataaga tgatattttt 300
 aaattatataa atgtcatcag gtccgaaaat aacgagaata tttcaatcttc tcataatgtt 360
 ggc当地ctgtt catgtgcatt gcttcataatacactggcg caaggagcgc cgc当地cgna 420
 gnntgcncgn cgncccacct nacccatgc cgaacttcag aantgaaaac nccntaacnc 480
 cgatngtcgg cgggngcctc cccatgcnan agtangggaa ntgc当地angcg ncnnattaaa 540
 cggaaaggctn attncaaaaga ctgggccttn ctttatctg atggttgc gagaacgctc 600
 tcctgagnan gacaaatncc gccgggagcg gatttgaacn t 641

<210> 450
 <211> 314
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(314)
 <223> n = A,T,C or G

<400> 450

gaactacgag	taagaatagc	tnogaattcc	cgttatgga	taacggcaaa	gggcttcgtt	60
tttcctata	cttattcagc	actcacaaat	aaaggaacgc	caatgaaaat	tatactctgg	120
gctgtattga	ttatttcct	gattgggcta	ctgggtgtga	ctggcgtatt	taagatgata	180
ttttaaaatt	aattaatgtc	atcaggctcg	aaaataaacga	aatatttca	gtctctcatc	240
ctgttgcgtc	cctgtcatgt	gcattgcttc	atataatcac	tggcgcaagg	agcgcgcagg	300
gggnntnnnt	cttt					314

<210> 451

<211> 236

<212> DNA

<213> Escherichia coli

<400> 451

atatacacta	agtgaatgat	atcttccgat	ttatcttaat	cgttatgga	taacggcaaa	60
gggcttcgtt	tttcctata	cttattcagc	actcacaaat	aaaggaacgc	caatgaaaat	120
tatactctgg	gctgtattga	ttatttcct	gattgggcta	ctgggtgtga	ctggcgtatt	180
taagatgata	ttttaaaatt	aattaatgtc	atcaggctcg	aaaataaacga	aatat	236

<210> 452

<211> 418

<212> DNA

<213> Escherichia coli

<400> 452

cggagattac	cgtgtgttgc	gatatatttt	ttagttcgc	gtggcaatac	atcagtggca	60
ataaaaacgac	atatccagaa	aaatatacac	taagtgaatg	atatcttccg	atttatctta	120
atcgttatg	gataacggca	aagggcttcg	tttttccta	tacttattca	gcactcacaa	180
ataaaaggaac	gccaatgaaa	attatactct	gggctgtatt	gattattttc	ctgattggc	240
tactgggtgt	gactggcgta	tttaagatga	tatTTaaaa	ttaattaatg	tcatcaggc	300
cggaaaataac	gagaatattt	cagtctctca	tcctgttgcg	ctcctgtcat	gtgcattgct	360
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<210> 453

<211> 551

<212> DNA

<213> Escherichia coli

<400> 453

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cgaccgcct	tcgactgtta	atgggcgaat	tttcagact	ggtatttaggt	ggacaacgcg	120
cgctgcctaa	acggctggaa	gaagcgggtt	ttgcgttgc	ctggtacgt	ttagaagagg	180
cgctggcgga	tgcgttgc	tgcgtgggtt	tacagcaaac	atccgcctgt	taactcccg	240
tgttacagga	ttagtggctt	tgcgcataa	gatcgtctgg	tgaaagtgcg	gtcaccatca	300
taactaactc	tctgtctaaa	cctctatcca	gcatctcctg	agcaatacgc	agggcttctt	360
cgtgttgc	ctgcattgcg	ccttcttac	gtaatctgc	agcaatggtc	atcaagttc	420
tcctttctt	gtggcgcg	ttccgcatac	tcaccaataa	atgcacgaaa	acgctggca	480
tcccctgttt	gtaatacgt	attaaacagg	gcttttagct	gtctgtcatt	agtgkccct	540
gtaactagca	g					551

<210> 454

<211> 93

<212> DNA

<213> Escherichia coli

<400> 454

tggcatctcg gtgttgcga tcttcatgat atccagcccc ccggaaactt cttccaaac	60
ggtttgctg ttatccattg agtcacggaa ctg	93
<210> 455	
<211> 232	
<212> DNA	
<213> Escherichia coli	
<400> 455	
cgtgccgaga tgatcctgta accatcatca gttgtgaagt agtgattcac gacttcaagg	60
cgctttcaa aagggtattt tgcttgac atattagggg ctattccatt tcatcgcca	120
acaaaatggg tgcagtacat actcgttgg aatcaacaca ggaggctggg aatggcgag	180
aaatatagat tactttctt aatagtgatt tgttcacgc ttttattttt ca	232
<210> 456	
<211> 713	
<212> DNA	
<213> Escherichia coli	
<220>	
<221> misc_feature	
<222> (1)...(713)	
<223> n = A,T,C or G	
<400> 456	
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ccagcagagc gcggcccttct tcgtcagatt tcgcagtagt ggtaatggta atatccaaac	120
caccaacgcg gtcgacttta tcgtagtcga tttctggaa gatgatctgc tcacggacac	180
ccatgctgta gttaccacga ccgtcgaaag acttagcgga caggccacgg aagtacggaa	240
tacgaggtac agcaatagtg atcaggcgct caaagaactc ccacatgcgt tcgcccacgca	300
gagttacttt acagccgatc ggatagccct gacggatttt gaagcctgca acagatttc	360
gtgcttttgt gatcagcggt tttgaccgg agattgctgc caggtctgct gctcggttat	420
ccagcagttt ttgtcagcg atcgcttcac caacacccat gttcagggtt atcttctcgaa	480
cccgaggggac ttgcatacaca gaattgttagt taaactcagt catgagtttt ttaactactt	540
cgtcttgcgt gtaatcatgc agtttcgcca tcgtactact ccatgtcggt gaacgctctc	600
ctgagtagga caaatccgccc ggagccggat ttaacgttgc gaacaaccgn cccggagggg	660
tggnggcagg accccgcccc aactggcagc attaaattaa gcagaaggcc atc	713
<210> 457	
<211> 292	
<212> DNA	
<213> Escherichia coli	
<400> 457	
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cctttaagga tatagaatag gggtagtact acgccagaat atcgtatttg attattgcta	120
gttttagtt ttgtttaaaa atattgttag ttttataaaa tgcaaaaacta aattattggat	180
atcatgaatt tttgttatgt tgaataaaaat ataggggggat atagatagac gtcattttca	240
tagggtata aatgcgacta ccatgaagtt tttaattgaa agtattgggt tg	292
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<211> 282	
<212> DNA	
<213> Escherichia coli	
<400> 458	
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agggggtat agatagacgt catttcata gggttataaa tgcgactacc atgaagttt	120
taattgaaag tattgggttg ctgataattt gagctgtctt attctttta aatatctata	180
taggtctgtt aatggatttt attttacaa tttttgtgt ttaggcataat aaaaatcaac	240
cccccataatg aacggcggtt taaaatattt acaacttagc aa	282
<210> 459	
<211> 300	
<212> DNA	
<213> Escherichia coli	
<400> 459	
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ggggaaaggca aaattgtcctc tggttggaaagca ttgcgtgggg tccggcgctc atcaacaatc	120
ggggggcagc aaggggctga aacggggaaag cccctcccgaa agaagggggcc ttgtataagg	180
aaagggttat gatgaagctc gtcatcatac tggttgtgtt gttactgtta agtttcccgaa	240
cttactaaca actcatcaga ggggggagaa atcctccctt acccttgcgtt ctttactcta	300
<210> 460	
<211> 293	
<212> DNA	
<213> Escherichia coli	
<400> 460	
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cccgaaaggaa gggccttgc taaggaaagg gttatgtatgc agctcgatc catactggtt	120
gtgttgcgttac tggtaagttt cccgacttac taacaactca tcagaggggg gagaatccct	180
cccttaccct tggcccttta ctctaggttgg aaaaaacaac agcgtcaata ggcctgccat	240
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<210> 461	
<211> 359	
<212> DNA	
<213> Escherichia coli	
<400> 461	
caacacagga ggctggaaat gcccgagaaa tatagattac tttctttat agtgatttgc	60
ttcacgctttt tatttttcac ctggatgata agagattcac tggatgttgcattt gcatattaaa	120
caggagagtt atgagctggc ggcgttttgc gcctgcaat tggaaagatgta agagtctcg	180
gcggggaaattt attcccgccct tacttacggc gttgcgttgcattt ctcattgcac ccaaatttat	240
tcttcacaaa aataataata gattttatata cgcgatcgat tatttttttc ctgaaaacaa	300
ataaaaaaaat ccccgccaaa tggcaggat ctttagattctt gtcgttttgc gcaagat	359
<210> 462	
<211> 673	
<212> DNA	
<213> Escherichia coli	
<400> 462	
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ggcttgaca tattaggggc tattccattt catcgccaa caaaatgggt gcagtgatcata	180
ctcggtggaa atcaacacag gaggctggaa atgcccggaga aatatacgatc acttttttttgc	240
atagtgtt gtttgcgtt ttttatttttc acctggatgc taagatgttgc actgtgtgaa	300
ttgcgttattt aacaggagat ttatgtatgc gggcggtttt tagcctgcata attgaaagat	360
taagagtctt cggcgaaaa ttattccgc cttacttacg ggcgttgcgc ttcttattgc	420
acccaaattt attcttcaca aaaataataa tagattttat tacgcgtatgc attatttttttgc	480
tcctgaaaac aaataaaaaaa atccccggca aatggcaggat atcttagattt ctgtgttttgc	540

aaggcagagaa tacaggctgg ttacgttacc agctgccggg ccttagcgc cgcttcgat
ggtaaggac actttctgac ctgcgtccag agattgtaa ccatcgttct ggatagcaga
gaagtgtacg aac 600
660
673

<210> 463
<211> 630
<212> DNA
<213> Escherichia coli

<400> 463
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caccacgggg gctaatacttg actctagacc actcaagaat agccgcgaaa cgttgtcatt 120
acaacacagg cggctatatg acgttcgcag agctggcat ggccttctgg catgatttag 180
cggtccggcattgtgc attcttgcca gtatgtatcgtaactggctg aacaagcgaa 240
agtaacgtgt catgcgggccc tcaggctgcc gtaatggcaa ttgcgcggc gaccaggccg 300
cagggggaa actctgcggc cttttcgtt cttactgcgg gtaaggcacc cagtcgcgc 360
cggtcaggcg aacgtacggt ttatccttgtt attgaataac tactgcattt gagttctcg 420
agaccgggtgc tgtttgccgc aaccactgg tgagttttt ccagtcaaca ttgtcttcgg 480
tgaaaatctt gccatcgaga acgcgaacca ccagatcgaa gatagccagg aagctgctcg 540
gttgcgtat gacaatcggt gccccctgat gcgggcctt catgcgaag aatttcaccc 600
caacggggac gtcgggtata gacgggctag 630

<210> 464
<211> 391
<212> DNA
<213> Escherichia coli

<400> 464
ctcaggctgc tgattgtttt ttgtgcaat ggcgcgttat tagcgtcgat gctgtcgatg 60
gagagaatca taaacgttgtt gaatgtatgtat tgtagcaag gaaaactgtc aaaaatcttc 120
aaaaaatggaggataagg ccggaatggc tccggccaga gggaaatggaa ccgcgaagct 180
gttgcgtctt gagggtcgat ttaaccagac gccaggcgct ccatacgcca aaaccgcgtc 240
tggcccgccg gaccagcata ttaggatggc gaatcgatcca gatcgccatc acgctactgc 300
caaccagcgc ccaggagcgc agacttagca gcatattcca ggcgcgtatcg taagcgctg 360
ttgtctccat ccattcacga cgactggcg a 391

<210> 465
<211> 625
<212> DNA
<213> Escherichia coli

<400> 465
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gtactggaa taattttatt ttctggttt ctggccgcgt atttcagcca caaatggat 120
gactaatgaa cggagataat ccctcaccta accggccctt ttttacagtt gtgtacaagg 180
ggcctgatatt ttatgacggc gaaaaaaaaac cgccagtaaa cccggcggtga atgctgtcat 240
ggatagattt gtgtttgtt tttacgctaa caggcattt cctgcactga taacgaatcg 300
ttgacacagt agcatcgtt ttctcaatga atgttaaacg gagcttaaac tcggtaatc 360
acatttgtt cgtcaataaa catgcagcga ttctccgg tttgcttacc ctcatacatt 420
gccccgtccg ctcttccat gaccacatcc agaggctt caggaaatgc ggcactcaca 480
cctgctgtca cggtaatgtt gatatgcct tcagaatgtg ttagggcatg gttatcgact 540
aactggcaaa ttctgacacc tgcacgacat gcttcttcat cattagccgc tttgacaata 600
atgataaatt ctgcggccccc gtagc 625

<210> 466
<211> 623
<212> DNA

<213> Escherichia coli

<400> 466

tgctttgaa tatgtgctcg caatctttag aaggaaatgg cgaccacgaa agaaaaggca	60
aaaacgataa tctgaaagag ccaaggtatt tcagtataag cattgaatgc gacagtaaac	120
tcttcggta tcagccagag agtgagacca aaaatgataa tcgtatacat aagtcttcg	180
agtggctcgt tagcaaaaag tttcaacaat ggagtaata catccaacat atcaataact	240
ctcaactgta agggatttga aatgttaaca caagctctcg ctgttaggggt atagccgaga	300
ccaccgaagc ccggagggtgg taaaataaaaa ccgggcacaa cacgaaggcg catttccat	360
atccataaaag agtcggctt gtctgttaaa tttaaatggt gggagtgcgc ctccggttgt	420
aaataacgac attgctgtgt gtgtcctgg cggcatcagt tttttctt aagttcggct	480
gatgtccgcc ctttttaaaag tgaattttgt gatgcggta atgcggctaa ggcacgtgg	540
cacagttaaa agtcatgtt gtccttattt gtttgggtgg gaaagccgac tgtaatttgg	600
aactgggtgc agtcacctgg agg	623

<210> 467

<211> 234

<212> DNA

<213> Escherichia coli

<400> 467

tgtttactta caagagattc atctttgtat aaataaaagat aagtaattac gcataaaaaca	60
acaatgatta taatagcaaa aataaatatt atcatcttt atagattact tgagatagcc	120
agcatcttgtt aaagccttta tcgtttttt atgctctgga ttaatataat cactacatct	180
atctgagcaa tctgttggt atggacatgtt caacccatgg tcatttacag ccaa	234

<210> 468

<211> 529

<212> DNA

<213> Escherichia coli

<400> 468

attagctatt tcggctaaaa tagagactac atgtcttcgg tccatctcac ttaaggagtg	60
tagttccgtt gtaagttttt ccatagctt cactgctaaa ttcaacaa ggaattttct	120
gctggtaatc tctaaaaaga tgccatggtt tacaatgatt ttgtttccct ttgttattt	180
atgaacaact gtccatgatt tcgtttaaga atgaagagaa atcactaaac gaactgaata	240
tattttctgt gccaatattt tctctaattt caaaaaagtt acttttataatg tcggtaatga	300
ctccaactta ttgatagtgt ttatgttca gataatgccc gatgacttt tcattcagct	360
ccaccgattt tgagaacgac agcgacttcc gtcccaagcc tgccaggtgc tgccctcagat	420
tcaggttattt ccgctcaattt cgctcgat atcgctttt cttatcattt cgttgatgtc	480
agtggttttt accacgaggg agcttcacgc gagttattga aaaccctga	529

<210> 469

<211> 261

<212> DNA

<213> Escherichia coli

<400> 469

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aattaatgca attatcgaaa attcaaaaaa tatccaaaaa tagtataactt tattccagaa	120
gagttcaata taatgtttgtt cttcaatttt tcttacttca ggtaatata gattgctcat	180
tacattgtga gcttcattt tatttaattt tctgttactt ccagctctcc gtgataacgg	240
ttttataattt agatgcttat c	261

<210> 470

<211> 98

<212> DNA

<213> Escherichia coli

<400> 470

agatgattgc cggyaacttg ttagcggcac gcaggcgcg gctgcaccc ttaccctgct 60
cttacgtac ttctgcgttg atagtaaaca tttcttc 98

<210> 471

<211> 259

<212> DNA

<213> Escherichia coli

<400> 471

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agctttaact ttgatttctt taccgtcaac aacgtatggc agaacttcgc tgtagaattc 120
agctttagct tgcgttca tgactttgtc gtgatccagc tcgatagcca gcggcgcttc 180
tttgccaccg tagatgattt ccgggaactt gttagcggca cgcaggcgcc ggctcgcacc 240
cttaccctgc tctttacgt 259

<210> 472

<211> 94

<212> DNA

<213> Escherichia coli

<400> 472

aaaaaacggcg taaagaaaagg atgcaaacat gttataaaaa actcaaattt atcccacgta 60
tatattacgc cgcaaaatcc ttacaataaa cagg 94

<210> 473

<211> 174

<212> DNA

<213> Escherichia coli

<400> 473

ttaattatta aaatagtgtt acgcgattat gtggttatgg gggtaaacat taaataaacc 60
agcggggagg ggaggttaaag tgaaaaata aaaagcggat aatctaata agcaggccgg 120
acagcatgc catccggcac tgatacgagg tttatttcag ctcatcaacc atcg 174

<210> 474

<211> 138

<212> DNA

<213> Escherichia coli

<400> 474

ctgtaaaaac gtcaaaaaga gtgtttatc aacagaagaa tggaggtctg acagatagta 60
gtaatgc当地aaaatggaga cttaagtta atgaacggga gtaaagcgaa aagactata
agtgaaggag aaattcccc 120
138

<210> 475

<211> 191

<212> DNA

<213> Escherichia coli

<400> 475

tttgtggct taatattcta ttgttatctt tatttataga tgtttatatt gcatgaggtg 60
gttttggag agaagaatga ggaagatgcg tcgagccaca gaaacgttag ctttacatat 120
agcggaggtg atgtgaaatt aatttacaat agaaataatt tacatatcaa acagtttagat 180
gcttttgc g 191

<210> 476
 <211> 245
 <212> DNA
 <213> Escherichia coli

<400> 476
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 tatctcgtaa aatgttcctg cccaaactgc acccaagagt cagaacacag ttttcaaga 120
 gtacaaaaag gtgcccttt gatctgccct cattgcaaca aagtattcca gacaatctt 180
 aaagctgttag cctgattgtat ttatttagta acaagtattt ttatatttt aataatata 240
 ttaaa 245

<210> 477
 <211> 319
 <212> DNA
 <213> Escherichia coli

<400> 477
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 tcttgaggat cttaactcc ccacatttg tgaaagtat tcataaaaa aggaaggttg 120
 aataatttgt cttaataat cggcagtggaa gaatttagtaa aacgattaaa ttctactaaa 180
 tcattaaacgt aatcccataat atatttatca ttggatgaa aaatatgtgc accatattta 240
 tgaatctggaa taccctcaca gtcctctgtg tacgcatttc caccgatatg attttttc 300
 tcaatcacta aaactttt 319

<210> 478
 <211> 149
 <212> DNA
 <213> Escherichia coli

<400> 478
 cgagtatcg aagcgatgac gaagtgtatg gaaaaatcg aaaaactcg caaatcctga 60
 tgactttcgc cggacgtcag gccgccactt cggtgcgggtt acgtccggct ttcttgctt 120
 tgtaaagcgc caaatctgcc gatttcaac 149

<210> 479
 <211> 330
 <212> DNA
 <213> Escherichia coli

<400> 479
 gaaagtatct tcgttattga catcaactggaa aaataact tgctttcat tattaaactc 60
 gaagcgcgta ccgtatctgg acaaacattt atcgagctta ccaaattcct gaagaggttt 120
 aactacagat aacatttgcg cgtccttgc agtaatgccc gtcaaattcct tgacgggcat 180
 tatttagatt aaattaccag tatttctcg gagtgaagaa tattaccagg tatatttaac 240
 acccacgttc gcggaccagt cttgatctac gtcaccacca ccgaggtatg tagcatcggt 300
 ataggcgctg aagttcttgg tgaagctaaa 330

<210> 480
 <211> 191
 <212> DNA
 <213> Escherichia coli

<400> 480
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 actacgtggc gacgaccggg agatgtcggt ttacattaa caactgccat tgtattactc 120

ctccgactta ctcagcgccg ccaacgaagt ccagattctg gccttcttc agggtgacgt	180
aagttttt c	191
<210> 481	
<211> 188	
<212> DNA	
<213> Escherichia coli	
<400> 481	
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cagcttgat ttctgcttg gtcgcgtctt tagcaactt gagtacgatg gtgtggatt	120
tttccatcgc agtagacgct tttcagaaa cgtgcggtgc acgcagcacc ttcagcagac	180
gttcttca	188
<210> 482	
<211> 172	
<212> DNA	
<213> Escherichia coli	
<400> 482	
caaaggcgaa caaaggctgt gaagccgaa ggctccacag acagtgtac ttgaaggcct	60
tactgttct tcttaggagc gagcaccatg atcatctggc ggccttcgat ctgcgttggg	120
aaggattcga ccactgccag ttcttgcaaa tcgtcttca cgcgattaag ca	172
<210> 483	
<211> 266	
<212> DNA	
<213> Escherichia coli	
<400> 483	
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gaactgatcc gctttctgtct tcagttctg aactgatagc gaaaaacgtaa ttaaggccta	120
agagcacact actcttagcc cttaaacatt taacgcatttgc tcacgaactc ttctgcccggc	180
gttgggtgaa tggcgacggt attgtcgaag tctttttgg ttgccccat cttcagcgcc	240
accgcgaagc cctgcaacat ttcgtc	266
<210> 484	
<211> 259	
<212> DNA	
<213> Escherichia coli	
<400> 484	
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ttaaccgct gcacggtaac ctacaccaac cagctgcgc ttcttagtga agccttcggt	120
aacaccgata accattggat tcagcaggc acgcgcggta ccagcctgtg cccaaccgtc	180
tgcgttaacca tcacgcggac cgaaggtagt ggtattatct gcatgtttaa cttcaacagc	240
atcggtgaga gtacgagtc	259
<210> 485	
<211> 73	
<212> DNA	
<213> Escherichia coli	
<400> 485	
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ccgttaccg ggg	73